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GenCore version 5.1.6
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OM protein - protein search, using sw model

August 12, 2005, 14:04:14 ; Search time 20.2998 Seconds (without alignments) 483.460 Million cell updates/sec Run on:

US-09-758-308-2

536 1 VPHPNIEEVALSNTGEIPFY........LMTGFTGDFDSVIDCNTCVT 102 BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Scoring table: Sequence:

Title:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl: pir2:\* pir3:\* PIR 79:\* 1 2 K 4 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		٠			SOMMENTES	
Result	9700	Query	Length	Ë	ID	Description
2				1		
1		98.0	3010	Н	GNWVCJ	genome polyprotein
7		96.0	3010	-	A45573	
m	507.5	94.7	3010		GNWVTC	genome polyprotein
4		94.1	216	7	S21337	
ß		93.0	3010	Н	S18030	genome polyprotein
9		92.8	3011	Н	GNWVC3	
7	493.5	92.1	3010	-	GNWVTW	genome polyprotein
80	492.5	91.9	386	~	S68016	ATPase/RNA helicas
σ	•	91.9	3011	Н	S40770	genome polyprotein
10		91.3	3011	-	GNWVCH	
11		85.4	3033	-	JQ1303	genome polyprotein
12	446.5	83.3	876	7	PC2219	
13	442.5	82.6		-	GNWVJ8	genome polyprotein
14	381.5	71.2	m	-	JC5620	genome polyprotein
15	296.5	55.3	102	~	PC6028	genome polyprotein
16	260.5	48.6		~	T08839	ı
17	253.5	47.3		7	T08841	polyprotein - dour
18	99.	20.4		П	A44217	genome polyprotein
19	109.5	20.4	m	-	GNWVBV	genome polyprotein
20		19.5		-	GNWVHC	genome polyprotein
21	104.5	19.5	3898	-	GNWVHB	genome polyprotein
22	104.5	19.5	3898	~	S57437	$\mathbf{c}$
23	104	19.4	m	N	\$58295	•
24	101	18.8		~	A71223	hypothetical prote
25	101	18.8		~	B75191	
56	87.5	16.3	610	-	BVECRQ	н
27	87.5	•	611	~	F86069	_
28	87.5	16.3	611	7	H91222	_
29	87.5	16.3	166	7	H81794	ATP-dependent DNA

1357 VPHPNIEBVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 1416

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61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102

1 VPHPNIBEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA

ä 9

0; Indels 1; Gaps

98.0%; Score 525.5; DB 1; Length 3010; 99.0%; Pred. No. 9.7e-46; tive 0; Mismatches 0; Indels 1;

Query Match
Best Local Similarity 99.0
Matches 102; Conservative

ATP-dependent DNA	ATP-dependent DNA	hypothetical prote	hypothetical prote	ATP-dependent DNA	probable ATP-depen	DNA helicase XF138	hypothetical prote	DNA helicase TPS1	ATP-dependent DNA	probable helicase	ATP-dependent RNA	ATP-dependent RNA	ATP-dependent RNA	ATP-dependent RNA	hypothetical prote
G81216	AH0917	T24415	T04679	A10466	T35049	A82689	F70958	S50918	E82351	T34609	AF0216	B85749	690869	B64884	F86721
7	~	~	~	~	~	~	~	~	N	~	~	N	N	~	7
166	609	1231	926	610	731	645	212	1447	620	676	460	457	457	457	243
16.3	16.1	16.0	15.7	15.0	15.0	14.6	14.6	14.6	14.4	14.2	14.1	14.0	14.0	14.0	13.9
87.5	86.5	98	84	80.5	80.5	78.5	7.8	78	77	16	75.5	75	75	75	74.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

```
genome polyprotein - hepatitis C virus (strain J)
N;Contains: capsid protein C; envelope protein M; major envelope protein B; nonstructurr
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: A39253; PS0086
C;Accession: A39253; MulD:91088550; PMID:2175903
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: genomic RNA
A; Residues: 1-3010 (KTA:
A; Residues: 1-3010 (KTA:
A; Cross-references: UNIPROT: P26662; GB: D90208; NID: G221610; PIDN: BAA14233.1; PID: G22161¹
B; Kato, N.; Ohkoshi, S.; Shimotohno, K.
R; Kato, N.; Ohkoshi, S.; Shimotohno, K.
A; Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence vary
A; Reference number: PS0085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,
                                                                                                                                                                                                                                                                                                                                                A; Accession: A39253
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C;Date: 20-Feb-1995
C;Accession: S21337
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Best Local S
Matches 97
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Matches
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                                                                                                                     C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A45573
R;Tanaka, T:; Kato, N:; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Hijikata, Virus Res. 23, 39-53, 1992
A;Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: A;Reference number: A45573; MulD: 92295714; PMID:1318627
A;Reference number: A45573; MulD: 92295714; PMID:1318627
A;Residues: I-3010 cTAN>
A;Residues: UNIPROT:000269; GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1;
A;Residues: UNIPROT:000269; GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1;
A;Residues: UNIPROT:000269; GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1;
A;Residues: Targerimental source: HCV-JT
A;Note: sequence extracted from NCBI backbone (NCBIN:106207)
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C vir
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Cjacession: A38465
Rjakamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.;
J. Virol. 65, 1105-1113, 1991
A;Title: Structure and organization of the hepatitis C virus genome isolated from human A;Reference number: A38465; MUD:91140698; PMID:1847440
A;Accession: A38465
A;Molecule type: genomic RNA
A;Residues: 1-310 (-7AAs)
A;Cross-references: UNIPROT:P26663; EMBL:M58335; NID:9329770; PIDN:AAA72945.1; PID:93297
C;Superfamily: hepatitis C virus genome polyprotein glycoprotein; hydrolase; nonstructura
C;Keywords: AFP; capsid protein E #status predicted <CPC>
F;116-191/Product: capsid protein M #status predicted <CPC>
F;12-115/Product: capsid protein M #status predicted <CPC>
F;130-729/Product: nonstructural protein NS1 #status predicted <NS2>
F;130-1006/Product: nonstructural protein NS2 #status predicted <NS2>
F;1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
CF1007-1615/Product: nonstructural protein NS2 #status predicted <NS2>
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N.Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4s; nonstructural protein NS4b; nonstructural protein NS5
C; Species: hepatitis C virus
                                                          (nonstruct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1357 VPHPNIEEVALSNIGEIPFYGKAIPLEAIKGGRHLIFCHSKKKCDELAAKLSGLGINAVA 1416
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enome polyprotein - hepatitis C virus (strain JT)

1/Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)

protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

1/S. Species: hepatitis C virus

1/S. Species: hepatitis C virus

1/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
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95.1%; Pred. No. 1.3e-44;
ive 4; Mismatches 0.
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Best Local Similarity 95.1%;
Matches 98; Conservative
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F;1312-1317/Region: nucleotide-binding motif B
F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1616-1862/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q68968; EMBL:X65547; NID:g59494; PIDN:CAA46516.1; PID:g59495
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polvprotein
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C;Date: 19-May-2000 #sequence revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S18030; S33570; A48332; S18029
R;Honda, M.; Kaneko, S.; Massahi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A;Description: A whole genome of hepatitis C virus cDNA was isolated from a single patie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: genomic RNA
A; Residues: 1-3010 <HON>
A; Residues: 1-3010 <HON>
A; Residues: 1-3010 <HON>
A; Residues: 1-3010 <HON>
A; Crosa-references: Univerce: 196949; EMBL:X61596; NID:959478; PIDN:CAA43793.1; PID:959475
A; Crosa-reference: 1solate JK1 from an individual
B; Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
A; Honda, M.; Raneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
A; Honda, M.; Raneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
A; Honda, M.; Raneko, S.; Unoura, M.; Robayashi, K.; Murakami, S.
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A; Honda, M.; Raneko, S.; Unoura, M.; Robayashi, K.; Murakami, S.
A; Honda, M.; Raneko, S.; Unoura, M.; Robayashi, K.; Murakami, S.
A; Honda, M.; Raneko, S.; Unoura, M.; Robayashi, K.; Murakami, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1992
A;Description: A sentitive serodiagnosis of hepatitis C virus infection with two cloned
A;Reference number: S21336
A;Accession: S21337
                                                                                                                                                                                                                                                                                                                                                                                                                      ij
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: hepatitis C virus
C.Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
;1230-1237/Region: nucleotide-binding motif A (P-loop);1312-1317/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.1%; Score 504.5; DB 2; 94.2%; Pred. No. 8.4e-45; ive 2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                               Score 507.5; DB 1
Pred. No. 7.1e-44;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                        94.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 94.2 nes 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA A; Residues: 1-216 <SAT>
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Gaps

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F;2014-3011/Product: nonstructural protein NSS #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2077,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome polyprotein - hepatitis C virus (strain Taiwan)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004 C;Accession: A40244 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004 C;Accession: A40244 P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S. Virology 188, 102-113, 1992 A;Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92230206; PMID:1314449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;196,209,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
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                                                                                                                                             F;1316-1319/Region: DEXH motif
F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;730-1006/Product: nonstructural protein NS2 #status predicted <NS2>
                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 3011;
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Best Local Similarity 91.3%; Pred. No. 2e-42;
Matches 94; Conservative 5; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
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                                                                                                                                                                                                                                                                                                                                                               92.2%; Score 497.5; DB 1.
92.2%; Pred. No. 7.7e-43;
tive 3; Mismatches 4.
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C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: host Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                            95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: genomic RNA A;Residues: 1-3010 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
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A; Accession: FO0403
A; Molecule type: genomic RNA
A; Residues: 1577-1633 <CHA>
A; Cross-references: DBJ:D1028
A; Cross-references: DBJ:D1028
A; Cross-references: DBJ:D1028
A; Cross-references: DBJ:D1028
A; Experimental source: isolates E-b16
A; Accession: PQ404
A; Residues: 1577-1633 <CH2>
A; Experimental source: isolates E-b17
A; Residues: 1577-1633 <CH2>
A; Experimental source: isolates E-b17
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome protein; glycoprotein; hydrolase; nonstructura
F; 1-115/Product: capsid protein C #status predicted <CEPP>
F; 116-191/Product: capsid protein M #status predicted <EPP>
F; 116-191/Product: major envelope protein NS1 #status predicted <NES>
F; 192-389/Product: nonstructural protein NS1 #status predicted <NS1>
                                                                    A;Residues: 1547, T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOM>A;Residues: 1547, T',749-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOM>A;Cross-references: EMBL:X61591
A;Cross-references: EMBL:X61591
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TTC for residue 771 as Ser
A;Note: sequence extracted from NGBI backbone (NCBIN:121747, NCBIP:121748)
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: ATP: glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; serin F;2-115/Product: capsid protein C #status predicted <EPPA
F;10-191/Product: major envelope protein B #status predicted <NSI>
F;10-100/Product: nonstructural protein NSI #status predicted <NSI>
F;1007-1615/Product: nonstructural protein NSI #status predicted <NSI>
F;130-123/Region: nucleotide-binding motif A (P-loop)
F;1317/Region: nucleotide-binding motif A (P-loop)
F;1316-1317/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1683-2013/Product: nonstructural protein NS4b #status predicted <NB>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NSS>
F;204-3010/Product: nonstructural protein NS5 #status predicted <NSS>
F;196,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (Aq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            general polyprotein - hepatitis C virus (strain HCV-1)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS4s; nonstructural protein NS4b; nonstructural protein NS5
Species: hepatitis C virus
C; Species: hepatitis C virus
C; Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C; Accession: A39166; PQ0403; PQ0404
C; Accession: A39166; PQ0403; PQ0404
R; Choo, Q.L.; Richman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, C.; Coi Proc. Natl. Acad. Sci. U.S.A. 8451-2455, 1991
A; Title: Genetic organization and diversity of the hepatitis C virus.
A; Reference number: A39166; MUID: 91172826; PMID: 1848704
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A;Molecule type: mRNA
A;Residues: 1-3011 <CHO>
A;Residues: 1-3011 <CHO>
A;Cross-references: UNIPROT:P26664; GB:M62321; NID:G329873; PIDN:AAA45676.1; PID:G329874
A;Cross-references: UNIPROT:P26664; GB:M62321; NID:G329873; PIDN:AAA45676.1; PID:G329874
B;Chan, S.W.; McOmish, F.; Holmes, B.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.L
J. Gen. Virol. 73, 1131-1141, 1992
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Pred. No. 6.1e-43;
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92.2%;
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es 95; Conservative
                                             A; Molecule type: genomic RNA
A; Residues: 1-547,'T',549-621
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F;1316-1319/Region: DEXH motif
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N;Contains:
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A.Accession: S40770
A.Accession: S40770
A.Molecule type: genomic RNA
A.Molecule type: genome to the hepatitis C virus genome.
A.Reference number: PC1284; MUID:91013116; PMID:2170712
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A;Residues: 1-513 cOK2>
A;Residues: 1-513 cOK2>
A;Cross-references: GB:000831; NID:g221511; PIDN:BAA00705.1; PID:g221512
C;Superfamily: hepatitis C virus genome polyprotein
C;Reywords: ATP; glycoprotein; hydrolase; nucleotide binding; P-loop; polyprotein; gerin C;Reywords: ATP; glycoprotein; Histatus predicted cEPN>
F;10-139/Product: envelope protein M #status predicted cMED>
F;30-729/Product: nonstructural protein NS1 #status predicted cNS2>
F;300-729/Product: nonstructural protein NS2 #status predicted cNS2>
F;103-1237/Region: nucleotide-binding motif A (P-loop)
F;1137/Region: nucleotide-binding motif B
                                                                                                                                         the hepatitis C virus ATPase/RNA
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C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S68016
R;Jin, L.; Peterson, D.L.
Arch. Blochem. Blophys. 323, 47-53, 1995
A;Title: Expression, isolation, and characterization of the hepatitis C virus AT;
A;Reference number: S68016; MUID:96019946; PMID:7487072
A;Reference number: S68016
A;Accession: S68016
A;Accession: S68016
A;Molecule type: mRNA
A;Molecule 1-386 <JIN>
A;Cross-references: UNIPROT:Q04045
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: nonstructural protein; nucleotide binding; P-loop; polyprotein
F;24-31/Region: nucleotide-binding motif B
F:86-21/Region: nucleotide-binding motif B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 YYRGLDVSVIPSSGDVVVVATDALMTGFSGDFDSVIDCNTCVT 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 91.9%; Score 492.5; DB 2.
1. Similarity 91.3%; Pred. No. 2.8e-43; 94; Conservative 4; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome polyprotein - hepatitis C virus N;Contains: capsid protein C; envelope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F,90-93/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 94; Conserv
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Gaps

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Indels

Conservative

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yenome polyprotein - hepatitis C virus (strain H)
4,Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O
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A; Cross-references: UNIPROT: P27958; GB: M67463; NID: g329737; PIDN: AAA45534.1; PID: g329738
A; Cross-references: UNIPROT: P27958; GB: M67463; NID: g329737; PIDN: AAA45534.1; PID: g329738
R; Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
A; Title: Genomic structure of the human protorype strain H of hepatitis C virus: compari
A; Reference number: A41546; MUID: 92052256; PMID: 1658800
A; Reference number: A41546; MUID: 92052256; PMID: 1658800
A; Reference number: A41546; MUID: 92052256; PMID: 1658800
A; Note: neither amino acid nor nucleotide sequence is given
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP: Capsid protein C #status predicted <EPP>
F; 115. Pproduct: capsid protein C #status predicted <MED>
F; 115. Pproduct: monstructural protein NSI #status predicted <NSI>F; 130-1006/Product: nonstructural protein NSI #status predicted <NSI>F; 1100-115/Product: nonstructural protein NSI #status predicted <NSI>F; 1100-115/Product: nonstructural protein NSI #status predicted <NSI>F; 1100-115/Product: nonstructural protein Mill #status predicted <NSI>F; 1112-1117/Region: nucleotide-binding motif A (P-10op)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructur
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Kurai, K.; Iizuka, H.; Machida, A.; Miyakawa, Y. J. Gen. Virol. 72, 2697-2704, 1991
A;Title: Nucleotide sequence of the genomic RNA of hepatitis C virus isolated from a hum A;Reference number: JQ1303; MUID:92044440; PMID:1658196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A36814, A41546
R;Inchauspe, G; Zebedee, S; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992
A;Description: Genomic structure of the human prototype strain H of hepatitis C virus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1357 VSHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKCDELAAKLVALGINAVA 1416
9
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C;Accession: JQ1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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1 Similarity 91.3%; Pred. No. 5.2e-42;
94; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1417 YYRGLDVSVIPTSGDVVVVSTDALMTGFTGDFDSVIDCNTCVT 1459
                                                                                                                                                                                                  1417 YYRGLDVSVIPTSGDVVVVVATDALMTGYTGDFDSVIDCNTCVT 1459
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                                                                                                                                            YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT
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genome polyprotein - hepatitis C virus (strain HC-J8)
N;Contains: capsid protein C; envelope protein M; hepacivirin (BC 3.4.21.98) (nonstructuoring total mostructural protein NS4s, nonstructural protein NS5s; nonstructural protein NS5s; nonstructural protein NS5s; protein NS4s, nonstructural protein NS5s; proteins: hepatitis C virus
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C;Date: 31-Dec-1992 #sequence revision 31-Dec-1992 #text_change 09-Jul-2004
C;Date: 31-Dec-1992 #sequence NS: i Lizuka, H:; Tanaka, T.; Fukuda, S., Virology 188, 331-341, 1992
Virology 188, 331-341, 1992
A;Title: Full-length sequence of a hepatitis C virus genome having poor homology to represent mumber: A40250; MUID:92230232; PMID:1314459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: genomic RNA
A; Residues: 1-3033 cOKA>
A; Cross-references: UNIPROT: P26661; GB: D10988; GB: D01221; NID: G221608; PIDN: BAA01761.1;
R; Chan, S; W.; McOmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.?
J. Gen. Virol. 73, 1131-1141, 1992
A; Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to A; Reference number: PQ0393; MUID: 92268871; PMID: 1316939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Mcceule type: genomic RNA
A; Residues: 2678-2754 < CHA>
A; Residues: 2678-2754 < CHA>
A; Residues: 2678-2754 < CHA>
A; Cross-references: DBJ1010134
A; Experimental source: isolate B-bl2
B; Kato, N.; Octsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohns Biochem. Biophys. Res. Commun. 181, 279-285, 1991
A; Title: Distribution of plural HCV types in Japan.
A; Reference number: PQ0554; MUID:92068204; PMID:1720309
A; Accession: PQ0559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 2678-2729 < KAT>
A; Cross-references: GB:D10562; GB:D90518; NID:g221523; PIDN:BAA01418.1; PID:g221524
A; Cross-references: GB:D10562; GB:D90518; NID:g221523; PIDN:BAA01418.1; PID:g221524
A; Cross-references: GB:D10562; GB:D90518; NID:g221523; PIDN:BAA01418.1; PID:g221524
C; Superfamily: hepatidis C virus genome polyprotein
C; Keywords: ATP; capaid protein; envelope protein; glycoprotein; hydrolase; nonstructur
F;1-115/Product: capaid protein C #status predicted < CPC>
F;101-1919/Product: major envelope protein B #status predicted < NSI>
F;390-733/Product: nonstructural protein NSI #status predicted < NSI>
F;101-1619/Product: nonstructural protein NSI #status predicted < NSI>
F;111-1619/Product: nonstructural protein NSI #status predicted < NSI>
F;111-1613/Product: nucleotide-binding motif B
F;1316-1321/Region: nucleotide-binding motif B
F;1316-1321/Region: nucleotide-binding motif B
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F;1620-1866/Product: nonstructural protein NS4a #status predicted <N4A>
F;1867-2017/Product: nonstructural protein NS4b #status predicted <N4B>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F;2018-3033/Product: nonstructural protein NS5 #status predicted <NS5>
F;205,209,233,299,305,417,423,430,448,477,534,542,558,578,627,649,1091,1217,1259,2038,2
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstruct
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JC5620
R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 PHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVAY
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Matches 85; Conserv
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N;Contains: core protein; E1 (carboxyl end); E2/NS1 (amino end); NS3 protein; NS4A prote C;Species: hepatitis C virus (type 5a) (fragments)

C;Species: hepatitis C virus

C;Species: hepatitis C virus

C;Accession: PC2219

R;Stuyver, Li, Arnhem, W.V.; Wyseur, A.; Maertens, G.

Biochem. Biophys. Res. Commun. 202, 1308-1314, 1994

A;Title: Cloning and phylogenetic analysis of the core, E2, and NS3/NS4 regions of the A;Reference number: PC2219; MUID:94338342; PMID:7520237

A;Accession: PC2219

A;Molecule type: mRNA

A;Reference number: PC2219; MUID:94338342; PMID:7520237

A;Accession: PC2219

A;Molecule type: mRNA

A;Reference serum

C;Superiamily: hepatitis C virus genome polyprotein

C;Superiamily: hepatitis Predicted <NSR>

F;191-70/Product: B2/NSI (amino end)

F;12-783/Product: NS3 #status predicted <NSR>

F;339-411/Region: NS1 #status predicted <NSR>

F;338-410/Product: NS4B #status predicted <NSR>

F;338-410/Product: NS4B #status predicted <NSR>

F;338-410/Product: NS4B #status predicted <NSR>

F;388-876/Product: NS4B #status predicted <NSR>

F;388-876/Product: NS4B #status predicted <NSR>

F;388-876/Product: NS4B #status pr
A; Rolecule type: genomic RNA
A; Residues: 1-303 -00KA>
A; Rolecule type: genomic RNA
A; Residues: 1-303 -00KA>
A; Rolecule type: genomic RNA
A; Cross-references: UNIPROT: P26660; GB: D00944; NID: g221650; PIDN: BAA00792.1; PID: g221651
A; Experimental source: isolate HC-J6 from a Japanese individual
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: AFP; glycoprotein; hydrolase; P-loop; polyprotein; serine proteinase; transm
F; 2-115/Product: capsid protein C #status predicted <BPM>
F; 116-191/Product: envelope protein M #status predicted <BPM>
F; 130-133/Product: nonstructural protein NS1 #status predicted <NS2>
F; 130-133/Product: nonstructural protein NS2 #status predicted <NS2>
F; 1010-186/Product: nonstructural protein NS4 #status predicted <NAS>
F; 116-1321/Region: nucleotide-binding motif B
F; 1320-1323/Region: BEXH motif
F; 1670-1866/Product: nonstructural protein NS4 #status predicted <NAB>
F; 1018-1033/Product: nonstructural protein NS5 #status predicted <NAB>
F; 1018-3033/Product: nonstructural protein NS5 #status predicted <NAB>
F; 1018-3033/Product: nonstructural protein NS5 #status predicted <NAB>
F; 1018-3033/Product: nonstructural protein NS5 #status predicted <NAB>
F; 1018-2017/Product: nonstructural protein NS5 #status predicted <NAB>
F; 1018-3033/Product: nonstructural protein NS5 #status predicted <NAB>
F; 1018-2017/Product: nonstructural protein NS5 #status 
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85.4%; Score 457.5; DB 1; Length:
Best Local Similarity 86.3%; Pred. No. 1.1e-38;
Matches 88; Conservative 3; Mismatches 10; Indels
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82.4%; Pred. No. 3.9e-38;
ive 9; Mismatches 8;
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ground polyprotein - hepatitis GB virus C (fragment)
C;Species: hepatitis GB virus C
C;Species: hepatitis GB virus C
C;Species: 31-3an-1997 #sequence_revision 31-3an-1997 #text_change 09-Jul-2004
C;Accession: PC6028
R;Wang, X.T; Zhuang, H.; Li, H.; Fan, J.; Qi, Z.; Liu, G.
Chinese J. Microbiol. Immunol. 16, 263-266, 1996
A;Title: Detection of GBV-C infection and sequencing of partial gene of a Chinese strain A;Reference number: PC6028
A;Accession: PC6028
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A;Accesi
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(c) 1993 - 2005 Compugen Ltd.
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MEDILINE=9204440; PubMed=1658196; Okamoto H., Okada S., Sugiyama Y., Kurai K., Iizuka H., Machida A., Okada S., Sugiyama Y., Kurai K., Iizuka H., Machida A., Miyakawa Y., Mayumi M.; "Nucleotide sequences of the genomic RNA of hepatitis C virus isolated from a human carrier: comparison with reported isolates for conserved and divergent regions."; J. Gen. Virol. 72:2697-2704(1991).
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Kato N., Hijikata M., Ootsuyama Y., Nakagawa M., Ohkoshi S.,
Sugimura T., Shimotohno K.;
"Molecular cloning of the human hepatitis C virus genome from Japanese patients with non-A, non-B hepatitis.";
Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528(1990).
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Takamizawa A., Mori C., Fuke I., Manabe S., Murakami S., Fujita J.,
Onishi E., Andoh T., Yoshida I., Okayama H.;
"Structure and organization of the hepatitis C virus genome isolated
                                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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MEDLINE=92230232; PubMed=1314459;
MEDLINE=92230232; PubMed=1314459;
Mkamoto H., Kurai K., Okada S., Yamamoto K., Iizuka H., Tanaka T.,
Fukuda S., Tsuda F., Mishiro S.;
"Full-length sequence of a hepatitis C virus genome having poor homology to reported isolates: comparative study of four distinct genotypes.";
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MEDLINE=91172826; PubMed=1848704;
Choo Q., Richman K.H., Han J.H., Berger K., Lee C., Dong C.,
Gallegos C., Coit D., Medina-Selby A., Barr P.J., Weiner A.J.,
Bradley D.W., Kuo G., Houghton M.;
"Genetic organization and diversity of the hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
                                                                                                     Last sequence update)
Last annotation update)
   PRT; 1186 AA
                                                                      Created)
                                                                                                                                                                     Precursor polyprotein (Fragment).
Hepatitis C virus.
                                                               (TrEMBLrel. 01, C
(TrEMBLrel. 01, I
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J. Virol. 65:1105-1113(1991).
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   PRELIMINARY;
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            SEQUENCE FROM N.A.
MEDLINE=92230206; PubWed=1314449;
Chen P., Lin M., Tai K., Liu P., Lin C., Chen D.;
"The Taiwanese hepatitis C virus genome: sequence determination and mapping the 5' termini of viral genomic and antigenomic RNA.";
virology 188:102-113(1992).
                                                                                                             SEQUENCE FROM N.A.

MEDLINE=93323208; PubMed=8392606;

Hijikata M., Mizushima H., Akagi T., Mori S., Kakiuchi N., Kato N.,

Tanaka T., Kimura K., Shimotohno K.

"Two distinct proteinase activities required for the processing of putative nonstructural precursor protein of hepatitis C virus.";

J. Virol. 67:4665-4675(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.0%; Score 525.5; DB 2; Length 1186; 99.0%; Pred. No. 2.9e-45; ive 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                        Hijkbard M.;

Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.

R Wijkbard M.;

Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.

R MA1196; A61196; A61196.

R PIR; PS0329; PS0329.

R PDB; 1DX9; X-ray; A/B=305-491.

R PDB; 1DX9; X-ray; A/B=305-491.

R GO; GO:0009254; F:ATP binding; IEA.

GO; GO:000926; F:ATP-dependent helicase activity; IEA.

R InterPro; IPR00140; DEAD, Helicase C:

InterPro; IPR00140; DEAD, II.

R PFam; PF01006; HCV-NS44; I.

R PFam; PF01006; HCV-NS44; I.

R PFam; PF01006; HCV-NS44; I.

R PFAm; PF01001; HCV-NS44; I.

R PRAMT; SM00447; DEXDC; I.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2004 (TrEMBLrel. 26,
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Matches 102; Conservative
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Hepiticia C virus type 2.

Or Viruse; SRRA positive-strand viruses, no DNA stage; Flaviviridae; Branch positive-strand viruses, serRA positive control of the serVal viruses, serVal
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    This SWISS-PROT entry is copyright: It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                 631 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 690
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 24, Last sequence update)
025-OCT-2004 (Rel. 45, Last annotation update)
Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
Bnvelope glycoprotein El (GP32) (GP35); Envelope glycoprotein El
(GP48) (GP70) (NS1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.21.98); Nonstructural protein NS5A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
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MEDLINE=91088550; PubMed=2175903;
MEDLINE=91088550; PubMed=2175903;
Kato N., Hijikata M., Ootsuyama Y., Nakagawa M., Ohkoshi S.,
Sugimura T., Shimotohno K.;
"Molecular cloning of the human hepatitis C virus genome from Japanese patients with non-A, non-B hepatitis.";
Proc. Natl. Acad. Sci. U.S.A. 87:9524-9528(1990).
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-I-FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication.

-I-CATALVITI ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1'.

-I-CATALVITIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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SUBUNIT: The virion of this virus is a nucleocapsid covered by a lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus (isolate Japanese) (HCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                Length 2284;
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-!- SIMILARITY: Contains 1 peptidase U39 domain.
                                                                                                                                                                                                  Score 525.5; DB 2
Pred. No. 5.7e-45;
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                      NS4B.
NS5A.
NS5B.
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Potential.
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Best Local Similarity 99.0%;
Matches 102; Conservative
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NCBI_TaxID=11116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLG HCVJA
                                                                                                                                                           SEQUENCE
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      SIGNAL
                      CHAIN
                                                                                                                       CHAIN
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Coat protein; Core protein; Envelope protein; Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein; RNA-directed RNA polymerase; Serine protease; Transferase; Transferase; Instrumentane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellular aminopeptidase.
Capsid protein C (Potential).
Matrix protein (Potential).
Major envelope protein B (Potential).
Nonstructural protein NS1 (Potential).
Nonstructural protein NS2 (Potential).
Nonstructural protein NS2 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
There are no restrictions on
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Charge relay system (By similarity)
Charge relay system (By similarity)
ATP (Potential).
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N-linked
                                                                                                                                                                                                                                       InterPro; IPR002519; HCV_env.
InterPro; IPR002531; HCV_NS1.
InterPro; IPR00145; HCV_NS4a.
InterPro; IPR001490; HCV_NS4a.
InterPro; IPR002668; HCV_NS5a.
InterPro; IPR0021668; HCV_NS5a.
InterPro; IPR0021669; HCV_NS5a.
InterPro; IPR001650; Helicase C.
InterPro; IPR001650; Helicase C.
InterPro; IPR0010109; Pept_Ser_Cys.
InterPro; IPR0010109; Pept_Ber_Cys.
InterPro; IPR0010109; Pept_Bes_Sys.
InterPro; IPR001095; RNA_pol_DS_PS.
InterPro; IPR007095; RNA_pol_DS_PS.
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                                                                                                                                                                                                                              core
                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR007094; RNA_pol_Pfam; PF01543; HCV_capsid; 1. Pfam; PF01542; HCV_core; 1. Pfam; PF01539; HCV_env; 1. Pfam; PF01560; HCV_NS1; 1.
                                                                                              EMBL; D90208; BAA14233.1; -. PIR; A39253; GNWVCJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF01001; HCV NS4b; 1.
Pfam; PF01506; HCV NS5s; 1.
Pfam; PF00271; HelTcase_C; 1
Pfam; PF00999; Viral_RGRP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01538; HCV_NS2; 1
Pfam; PF02907; HCV_NS3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01006; HCV NS4a;
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7289
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                                                                                                                                                                                        InterPro; IPR001410;
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                                                                                                                                         LUXP.
                                                                                                                                                      MEROPS; S29.001;
MEROPS; U39.001;
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RA Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

BY Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

BY EMBL, AR2196; A61196.

BY PIR; PQ0224; PQ02246.

BY PIR; PQ0224; PQ0224.

BY PIR; PQ0224; PQ02254.

BY PIR; PQ0224; PQ02254.

BY PIR; PQ0224; PQ02254.

BY PIR; PQ0224; PROSCOSTA (NOV-1909) TEA.

BY GO; GO: 00109021; C: viral capsid; IEA.

GO; GO: 00109028; C: viral capsid; IEA.

GO; GO: 00109028; C: viral capsid; IEA.

GO; GO: 0008026; F: ATP-dependent helicase activity; IEA.

GO; GO: 0008254; F: RNA-directed RNA polymerase activity; IEA.

GO; GO: 0008256; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 0008256; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 0008256; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 0000826; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 0000826; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 0000826; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 0000826; F: PRA-directed RNA polymerase activity; IEA.

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GO; GO: 000826; F: PRA-directed RNA polymerase activity; IEA.

GO; GO: 000826; F
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InterPro; IPR009003; Pept Ser Cys.

DR InterPro; IPR002518; Pept_0139_HCV_NS2.

DR InterPro; IPR007094; RNA_pol_DS_PS.

DR Pfam; PF01543; HCV_core; 1.

DR Pfam; PF01542; HCV_core; 1.

DR Pfam; PF01539; HCV_ENV; 1.

DR Pfam; PF01539; HCV_NS2; 1.

DR Pfam; PF01539; HCV_NS2; 1.

DR Pfam; PF01509; HCV_NS2; 1.

DR Pfam; PF01001; HCV_NS4; 1.

DR Pfam; PF01001; HCV_NS4; 1.

DR Pfam; PF01506; HCV_NS4; 1.

DR Pfam; PF00190; CYTOCHROME C; UNKNOWN_1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

SQ SEQUENCE 3010 AA; 327024 MW; RATEDAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VPHPNIEEVALSNTGEIPPYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.0%; Score 525.5; DB 2; Length 3010; Best Local Similarity 99.0%; Pred. No. 7.5e-45; Matches 102; Conservative 0; Mismatches 0; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Hepatitis C virus.
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Q9J3H5
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                                                                                                                                                                                                                      0; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                          N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
N-linked (GlcNAc. ..) (Potential).
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R PIR; M61196; A61196.

R PIR; P00246; P00246.

R PIR; P00246; P00204.

R PIR; P00246; P00204.

R PIR; P0019031; Cintegral to membrane; IEA.

R O; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0019031; C:viral capaid; IEA.

GO; GO:0019031; C:viral capaid; IEA.

GO; GO:0003226; F:ATP-dependent helicase activity; IEA.

GO; GO:0003236; F:ATP-dependent helicase activity; IEA.

GO; GO:0003236; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0003239; F:Ruructural molecule activity; IEA.

GO; GO:0003299; F:ranscription; IEA.

GO; GO:000399; P:viral genome replication; IEA.

INTER-PRO; IPR00140; DEAD.

R InterPro; IPR00140; DEAD.

R InterPro; IPR002521; HCV core.

R InterPro; IPR002521; HCV NS4.

R InterPro; IPR001490; HCV_NS4.

R InterPro; IPR001409; Peptidase_S29.
                                                                                                                                                                         Query Match 98.0%; Score 525.5; DB 1; Length 3010; Best Local Similarity 99.0%; Pred. No. 7.5e-45; Matches 102; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                         3010 AA; 327017 MW; AA993794F46DB185 CRC64;
                                                                                                                                                                                                                                                                                                                                                   61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=type 1b;
Tanaka T.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; D89872; BAA14035.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANAKA T.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MXY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
1-MAY-1997 (TrEMBLrel. 26, Last annotation update)
RNA for polyprotein, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 3010 AA
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                                             2041
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NCBI_TaxID=11103;
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TANAKA T.;
                                                                                                            CARBOHYD
SEQUENCE
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CARBOHYD
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NCBI_TaxID=11103;
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AC 068K
AC 068K
DT 25-0
DT 25-0
DT 25-0
DT 25-0
DC Hepa
CC Hep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VPHPNIEEVALSNTGEIPPYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLMAVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Hepatitis C virus (HCV) genotype 1b sequences from fifteen patients with hepatocellular carcinoma: the 'progression score' revisited."; Hepatol. Res. 20:161-171(2001).
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
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Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
Mishiro S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1417 YYRGLDVSVIPTSGDVVVVATDALMTGFTGFFDSVIDCNTCVT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3010 AA; 326803 MW; 9FEE3D1B93B7AA4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 519.5; DB 2
Pred. No. 3.1e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                            InterPro; IPR001490; HCV_N34b.
InterPro; IPR001266; HCV_N34b.
InterPro; IPR001266; HCV_RGRP.
InterPro; IPR001669; Helicase_C.
InterPro; IPR00109; Peptidase_S29.
InterPro; IPR00109; Pept_Ser_Cys.
InterPro; IPR00218; Pept_3er_Cys.
InterPro; IPR007995; RNA_pol_DS_PS_INERPRO; IPR07094; RNA_pol_PS_VIY.
Pfam; PP01343; HCV_Capsid; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016021; C:integral to membr
GO; GO:0019028; C:viral capsid; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01539; HCV env; 1.
Pfam; PF01560; HCV NS1; 1.
Pfam; PF01560; HCV NS2; 1.
Pfam; PF02907; HCV NS3; 1.
Pfam; PF01001; HCV NS4a; 1.
Pfam; PF01001; HCV NS4b; 1.
Pfam; PF01001; HCV NS5a; 1.
Pfam; PF00271; Hellcase (2; 1.
Pfam; PF00998; Viral RGRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 96.9%;
Best Local Similarity 97.1%;
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB049088; BAB18801.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR, A61196, A61196.
PIR, PQ0246; PQ0246.
PIR, PQ0804, PQ0804.
PIR, PS0329; PS0329.
HSSP, Q8JYS1; ICWX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9DTE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
Q9DTE9
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1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00487; DEXDG; 1.
PROSTIE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
GO; GO:0019031; C:viral envelope; .....
GO; GO:000524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0005198; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:RNA-cural molecule activity; IEA.
GO; GO:0019079; P:RT anscription; IEA.
GO; GO:0019079; P:Viral ganome replication; IEA.
R InterPro; IPR001945; P:Viral transformation; IEA.
R InterPro; IPR001945; DEAD/DEAH N.
R InterPro; IPR001545; DEAD/DEAH N.
R InterPro; IPR001551; HCV_capsid.
DR InterPro; IPR002521; HCV_capsid.
DR InterPro; IPR002519; HCV_NS1.
DR InterPro; IPR002519; HCV_NS1.
DR InterPro; IPR001490; HCV_NS4.
DR InterPro; IPR001490; HCV_NS5a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1417 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 1459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3010 AA; 326780 MW; 668CFFEA5FEC3658 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q68K36;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 518.5; DB 2;
Pred. No. 3.9e-44;
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96.1%; Pred. No. 3...
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR002518; Pept U39 HCV N.
InterPro; IPR007095; RNA DOL DS PS.
InterPro; IPR007094; RNA DOL PSVir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01538; HCV NS2; 1. Pfam; PF01538; HCV NS2; 1. Pfam; PF02907; HCV NS4a; 1. Pfam; PF01006; HCV NS4b; 1. Pfam; PF01506; HCV NS5a; 1. Pfam; PF001506; HCV NS5a; 1. Pfam; PF00271; Halicase C; 1. Pfam; PF00998; Viral_RdRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01543; HCV capsid;
Pfam; PF01542; HCV core; 1
Pfam; PF01539; HCV env; 1.
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nes 99; Conservative
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Hepatitis C virus.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                           Hepatitis C virus
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                                                                                                                                                                                                                                Polyprotein.
                                                                                                                                                              Q9J3G8
Q9J3G8;
                                                                                                                                    RESULT 9
Q9J3G8
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A Kleiner D., Holman S., Augenbraun M., Taylor J.;
A Kleiner D., Holman S., Augenbraun M., Taylor J.;
T Sequence Analysis of Hepatitis C Virus Replication Functions in HCV/HIV Coinfected Subjects.";
Submitted (JUL_2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY68552; AAT94256.1;
IR InterPro; IPR01144; DEAD/DEAH N.
IN InterPro; IPR01144; DEAD/DEAH N.
InterPro; IPR01145; DEAD/DEAH N.
InterPro; IPR00145; HCV/NS4a.
InterPro; IPR001050; Helicase.
InterPro; IPR001050; Peptidase S29.
InterPro; IPR0010619; Peptidase S29.
InterPro; IPR0010619; Peptidase S29.
InterPro; IPR0010619; Peptidase.
IN Refam; PF02207; HCV/NS3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Kleiner D., Holman S., Augenbraun M., Taylor J.;

"Sequence Analysis of Hepatitis C Virus Replication Functions in
T "Sequence Analysis of Hepatitis C Virus Replication Functions in
T HCV/HTV Confected Subjects.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; AX68536; AAT94277.1; -
R InterPro; IPR00110; DEAD.

R InterPro; IPR00110; DEAD.

R InterPro; IPR00110; Peptidase C.
R InterPro; IPR00410; Peptidase S29.
R InterPro; IPR00410; Peptidase S29.
R InterPro; IPR004003; Peptidase S29.
R Pfam; PF02907; HCV NS3; 1.
R Pfam; PF02006; HCV NS4a: 1.
R Pfam; PF020071; Helicase C: 1.
R SMART; SM00490; HELICC; 1.
                                                                                                                                                                                                                                                                                                           1, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                              Query Match 96.5%; Score 517.5; DB 2; Length 659; Best Local Similarity 97.1%; Pred. No. 1.1e-44; Matches 100; Conservative 1; Mismatches 1; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                         61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                     312 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 354
                                                                                                                                                                                                                                                        70411 MW; 2FCC6D44A67324E1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             068K57;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 659 AA
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                                                                                                                                                                                                                                             629
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                                                                                                                                                                                                                                                          659 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                             629
                                                                                                                                                                                                                 Polyprotein.
NON_TER
NON_TER
6
SEQUENCE 65
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NON TER
SEQUENCE
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Pfam; PP01001; HCV NS4b; 1.
Pfam; PP01506; HCV_NS5a; 1.
Pfam; PP01506; HCV_NS5a; 1.
PR05199; Viral RdRP; 1.
PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; SUNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; SUNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; SUNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
PROSITE; PS00190; CYTOCHROWE C; UNKNOWN 1.
                                                                                                                                                                                                                                                                                       Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polyprotein (Fragment).
Hepatitis C virus.
                                                                                                                                                                                                                                                                Local Similarity
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25-OCT-2004
25-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepacivirus.
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                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                     1357 VPHPNIEBVALSNIGEIPPYGKAIPIEVIKGGRHLIFCHSKKKCDELAAKLSGLGLNAVA 1416
                                                                                                                                                                                                                                        1 VPHPNIBEVALSNTGEIPFYGKAIPIBAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 60
                                                                                                                                  Query Match 96.5%; Score 517.5; DB 2; Length 3010;
Best Local Similarity 97.1%; Pred. No. 5e-44;
Matches 100; Conservative 1; Mismatches 1; Indels 1; Gaps
             PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
Cost protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane,
SEQUENCE 3010 AA; 326863 MW; E0BEB3528215457C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=HCV-S;
Yuan Z., Mao H., Hu Y., Lan S., Wang H.;
"Construction of full-length complementary DNA of Hepatitis C Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polyprotein.
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R GO; GO: 0016021; C:integral to membrane; IEA.

R GO; GO: 0019028; C:viral capsid; IEA.

R GO; GO: 0019028; C:viral capsid; IEA.

R GO; GO: 0019021; C:viral capsid; IEA.

R GO; GO: 00019021; C:viral capsid; IEA.

R GO; GO: 00019026; F:ATP-dependent helicase activity; IEA.

R GO; GO: 00019123; F:RATP-dependent helicase activity; IEA.

R GO; GO: 00019123; F:RATP-dependent helicase activity; IEA.

R GO; GO: 00019129; F:RATP-dependent helicase activity; IEA.

R GO; GO: 00019136; F:RATP-dependent helicase activity; IEA.

R GO; GO: 00019136; F:RATP-dependent helicase activity; IEA.

R GO; GO: 00019139; P: structural molecule activity; IEA.

R GO; GO: 00019139; P: structural molecule activity; IEA.

R GO; GO: 0019139; P: structural molecule activity; IEA.

R GO; GO: 0019139; P: viral genome replication; IEA.

R InterPro; IPR001345; CytC_heme_BS.

R InterPro; IPR0013410; DEAD/DEAH N.

R InterPro; IPR001521; HCV_capsid.

R InterPro; IPR001521; HCV_core.

R InterPro; IPR001531; HCV_ene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zonomina Shi Yan He Lin Chuang Bing Du Xue Za Zhi 0:0-0(2004)
EMBL; AY460204; AAR22408.1; -.
HSSP; P26663; LJXP.
                                                                                                                                                                                                                                                                                                                                      05-UTL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR002166; HCV RARP.
InterPro; IPR001166; HCV RARP.
InterPro; IPR00118; Pept U39 HCV NS2.
InterPro; IPR007095; RNA pol DS PF.
InterPro; IPR007095; RNA pol PS PF.
PFam; PF01543; HCV capaid; 1.
Pfam; PF01543; HCV core; 1.
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InterPro; IPR001490; HCV_NS4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PP01542; HCV_core; 1.

PP01539; HCV env; 1.

PP01560; HCV NS1; 1.

PP01538; HCV NS2; 1.

PP01006; HCV_NS4a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O6SCJ5
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Qéscus
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1357 VPHPNIEEVALSNTGEIPFYGKAIPIETIKGGRHLIFCHSKKKODELAAKLSGLGLNAVA 1416
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                                                                                                                                1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
Parker M., Lamson D., Wroblewski D., Reilly A., Philpott S.,
A Kleiner D., Holman S., Augenbraun M., Taylor J.;
A Kleiner D., Holman S., Augenbraun M., Taylor J.;
A Kleiner D., Holman S., Augenbraun M., Taylor J.;
A Kleiner D., Dendritis C Virus Replication Functions in HCV/HIV Coinfected Subjects ";
Submitted (Jul_2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX68566; AAT94263.1; -.
INTERPRO; IPR01145; DEAD/DEAH_N.
InterPro; IPR01145; DEAD/DEAH_N.
InterPro; IPR01150; Peptidase_S29.
InterPro; IPR001050; Peptidase_S29.
InterPro; IPR001050; Peptidase_S29.
InterPro; IPR001050; Peptidase_S29.
InterPro; IPR00106; HCV_NS3; 1.
R Pfam; PF012071; HCV_NS3; 1.
R Pfam; PF010106; HCV_NS4; 1.
R Pfam; PF010171; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                   1;
96.5%; Score 517.5; DB 2; Length 3011; 97.1%; Pred. No. 5e-44; 1; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 96.4%; Score 516.5; DB 2; Length 659; Local Similarity 96.1%; Pred. No. 1.4e-44; les 99; Conservative 3; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                         61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               659 659
659 AA; 70519 MW; B48CCB1A0C6F9EDD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Polyprotein; Transmembrane.
                                                                                          Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus; Hepatitis C virus type 1.
NCBI_TaxID=31647;
                                                                                                                                                                                             EMBL, AF483269; AAL91977.1; -..

EMBL, A61196; A61196.

R PIR; PA61196; A61196.

R PIR; PA61196; A61196.

R PIR; PA61196; A61196.

R PASSP; Q807329; CONT.1; -..

R GO; GO:0019028; C:Viral capsid; IEA.

R GO; GO:0019031; C:Viral capsid; IEA.

R GO; GO:0019031; C:Viral envelope; IEA.

R GO; GO:00019028; F:ATP-dependent helicase activity; IEA.

R GO; GO:000326; F:ATP-dependent helicase activity; IEA.

R GO; GO:000326; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:000228; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:000529; F:Ructural molecule activity; IEA.

R GO; GO:0005509; F:proteolysis and peptidolysis; IEA.

R GO; GO:0005509; P:Viral genome replication; IEA.

R GO; GO:0019087; P:Viral genome replication; IEA.

R GO; GO:0019087; P:Viral genome replication; IEA.
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                                                                                                                                                         SEQUENCE FROM N.A.
Yildiz E., Oztan A., Akkiz H., Ozturk M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.4%; Score 516.5; DB 2; Best Local Similarity 96.1%; Pred. No. 6.3e-44; Matches 99; Conservative 2; Mismatches 1;
PRT; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004109; Peptidase S29.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR005109; Peptidase S29.
InterPro; IPR00518; Pept U39 HCV NS2.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007099; RNA pol DS PS.
Pfam; PP01543; HCV core; 1.
Pfam; PP01509; HCV NS1; 1.
Pfam; PP01001; HCV NS1; 1.
Pfam; PP01001; HCV NS48; 1.
Pfam; PP01001; HCV NS28; 1.
Pfam; PP00909; VIral RGRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPRO11545; DEAD/DEAH N. InterPro; IPR002522; HCV_capsid. InterPro; IPR002521; HCV_core. InterPro; IPR002519; HCV_core. InterPro; IPR002519; HCV_NS1. InterPro; IPR001745; HCV_NS4. InterPro; IPR001409; HCV_NS4D. InterPro; IPR001266; HCV_NS4D. InterPro; IPR002166; HCV_NS4D. InterPro; IPR002166; HCV_NS4D. InterPro; IPR002166; HCV_NS4D. InterPro; IPR002166; HCV_NSAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    GO, GO:0019087; P:viral transform:
InterPro; IPR000345; CytC_heme_BS
InterPro; IPR001410; DEAD.
                                                                                  Hepatitis C virus type 1b.
PRELIMINARY;
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SEQUENCE 30
                                                                      Polyprotein.
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STRAIN=HCV.N;
MEDLINE=99315771; PubMed=10385673; DOI=10.1002/hep.510300137;
Beard M.R., Abell G., Honda M., Carroll A., Gartland M., Clarke B., Suzuki K., Lanford R., Sangar D.V., Lemon S.M.;
"An infectious molecular clone of a Japanese genotype 1b hepatitis cvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepalitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Beard M.R., Abell G., Honda M., Carroll A., Gartland M., Clarke B.,
Suzuki K., Lanford R., Sangar D.V., Lemon S.M.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133594; AAD44718.2; --
HSSP; Q8JYS1; 1CWX.
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GO; GO: 0015021; C: ciral capsid; IEA.
GO; GO: 0015021; C: ciral capsid; IEA.
GO; GO: 0015524; F: ATP binding; IEA.
GO; GO: 0005526; F: RTP-dependent helicase activity; IEA.
GO; GO: 0003723; F: RNA binding; IEA.
GO; GO: 0003723; F: RNA directed RNA polymerase activity; IEA.
GO; GO: 0005566; F: RNA-directed RNA polymerase activity; IEA.
GO; GO: 0005198; F: Structural molecule activity; IEA.
GO; GO: 0005509; F: proteolysis and peptidolysis; IEA.
GO; GO: 000550; P: transcription; IEA.
GO; GO: 0019079; P: viral genome replication; IEA.
FO; GO: 0019079; P: viral transformation; IEA.
FO GO: 0019079; P: viral transformation; IEA.
                                                1417 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 1459
61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                        PRT; 3015 AA
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.00745; HCV.
.R001490; HCV.NSA.
IPR002166; HCV.NSA.
.J: IPR002166; HCV.NSA.
.J: IPR001650; HCICase C.
.erPro; IPR004109; Peptidase S29.
.nterPro; IPR004109; Peptidase S29.
.nterPro; IPR00518; Pept_U99HCV NS2.
.InterPro; IPR007094; RNA_Dol_Ds_FS.
.A InterPro; IPR007094; RNA_Dol_Ds_FS.
.A INTERPO; IPR007094; RNA_Dol_Ds_FS.
.A INTERPORTOR PNOS INTE
                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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InterPro; IPR001410; DEAD.
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InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatology 30:316-324(1999).
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
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HCV NS4b;
HCV NS5a;
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11103;
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                                                                                                                                                                                                                                                                                                                                                                            Q9WPH5;
                                                                                                                                                                                                                                                                                                                            Q9WPH5
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Pfam;
Pfam;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92295714; PubMed=1318627; DOI=10.1016/0168-1702(92)90066-1;
MEDLINE=92295714; PubMed=1318627; DOI=10.1016/0168-1702(92)90066-1;
A Hijkata M., Ishimura Y., Shimotohno K.;
Tuhikata M., Ishimura Y., Shimotohno K.;

"Molecular cloning of hepatitis C virus genome from a single Japanese carriats: sequence variation within the same individual and among ratifacted individuals.";

"Infected individuals.";

"Virus Res. 23:39-53(1992).

"Infected individuals.";

"Virus Res. 23:39-53(1992).

"Infected individuals.";

"Virus Res. 23:39-53(1992).

"Infected individuals.";

"Infected individuals...

"Infected indivi
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 45, Last sequence update)
02-67-2004 (Rel. 45, Last amnotation update)
03-67-2004 (Rel. 45, Last amnotation update)
04-07-2004 (Rel. 45, Last amnotation update)
05-07-2004 (NS1); Protein Pr) (RPS); Envelope glycoprotein B2
05-07 (NS1); Protein Pr) Nonstructural protein NS4 (Pr) (Hepacivirin)
05-07 (Rel. 47, 22, 199); Nonstructural protein NS5 (Pr); Nonstructural Protein 
                                                                                                                                                                                                                                                                                                                                   1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                                                                                                                                    Gaps
Pfam; PF00271; Helicase C; 1.
Pfam; PF00998; Viral RdRP; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; SP019protein; Transmembrane.
SEQUENCE 3015 AA; 326625 MW; A86AE71196578EE3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (RNA)(N).
SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                            Length 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1418 YYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVT 1460
                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                               DB 2;
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-1- SIMILARITY: Contains 1 peptidase U39 domain.
                                                                                                                                                                                                                            Score 516.5; DB 2
Pred. No. 6.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3010 AA
                                                                                                                                                                                                                                                                                 3; Mismatches
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                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.1%;
Matches 99; Conservative
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callular aminopepidase.
Capsid protein (Potential).
Matrix protein (Potential).
Major envelope protein E (Potential).
Nonstructural protein NS1/E2 (Potential).
Nonstructural protein NS2 (Potential).
Protease/helicase NS3 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding, Cat protein; Core protein; Envelope protein;
Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Serine protease; Transferase;
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                                                         InterPro; IRR002531; HCV_NS1.
InterPro; IRR00145; HCV_NS4.
InterPro; IRR00145; HCV_NS4.
InterPro; IRR00166; HCV_NS4.
InterPro; IRR00166; HCV_RGRP.
InterPro; IRR00166; Helfcase_C.
InterPro; IRR001691; Helfcase_C.
InterPro; IRR001903; Pept_Ser_Cys.
InterPro; IRR001903; Pept_Ber_Cys.
InterPro; IRR001903; Pept_Ber_Cys.
InterPro; IRR001095; RNA_pol_DS_PS.
InterPro; IRR001095; RNA_pol_DS_PS_IR.
               capsid
                                                                                                                                                                                                                                          Pfam; PF01543; HCV cappid; 1. Pfam; PF01543; HCV cappid; 1. Pfam; PF01542; HCV core; 1. Pfam; PF01550; HCV NS1; 1. Pfam; PF01550; HCV NS2; 1. Pfam; PF02907; HCV NS3; 1. Pfam; PF01001; HCV NS4b; 1. Pfam; PF01001; HCV NS4b; 1. Pfam; PF01501; HCV NS5a; 1. Pfam; PF01501; HcV NS5a; 1. Pfam; PF00299; Viral_RARP; 1. Pfam; PF00999; Viral_RARP; 1.
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                           InterPro; IPR002521; HCV_core.
InterPro; IPR002519; HCV_env.
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InterPro; IPR001410;
InterPro; IPR002522;
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BMBL; AP207765; AAF65946.1; --
PIR; A61196; A61196.
PIR; PQ0246; PQ0246
PIR; PQ08044; PQ0804.
PIR; PS0329; PS0329.
HSSP; Q8JYS1; 1CWX.
                                                              1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                 Viruses; BSRNA positive-strand viruses, no DNA stage; Flaviviridae;
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral capsid; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:00003526; F:ATP-dependent helicase activity; IEA.
GO; GO:00003526; F:RNA binding; IEA.
GO; GO:0000358; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:00005189; F:structural molecule activity; IEA.
GO; GO:0006508; P:proteclyals and peptidolysis; IEA.
GO; GO:0006508; P:transcription; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
Score 514.5; DB 1; Length 3010;
Pred. No. 1e-43;
4; Mismatches 0; Indels 1;
                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein.
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GO; GO: 0000723; F:ATP-dependent heli
GO; GO: 00003723; F:RNA-directed RNA p
GO; GO: 00003968; F:RNA-directed RNA p
GO; GO: 00008236; F:Berine-type peptid
GO; GO: 00005198; F:Berine-type peptid
GO; GO: 0005198; F:Berine-type peptid
GO; GO: 0001907; P:Viral genome replid
GO; GO: 001907; P:Viral genome replid
GO; GO: 001907; P:Viral genome replid
GO; GO: 001907; P:Viral transformatid
InterPro; IPR001410; DEAD/DEAH N.
InterPro; IPR001521; HCV_core.
InterPro; IPR002519; HCV_env.
InterPro; IPR002519; HCV_env.
InterPro; IPR0007519; HCV_NS4.
InterPro; IPR0007519; HCV_NS4.
InterPro; IPR0007688; HCV_NS4.
InterPro; IPR001688; HCV_NS4.
InterPro; IPR001688; HCV_NS5.
InterPro; IPR001688; HCV_NS5.
InterPro; IPR001688; HCV_NS5.
Query Match
Best Local Similarity 95.1%;
Matches 98; Conservative
                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=MD15;
                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                   Hepacivirus.
NCBI_TaxID=11103;
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completed: August 12, 2005, 14:21:19 ne: 96.231 secs

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August 12, 2005, 14:00:18 ; Search time 107.012 Seconds (without alignments) 368.645 Million cell updates/sec
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536
1 VPHPNIEEVALSNTGEIPFY......LMTGFTGDFDSVIDCNTCVT 102
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aar25736 HCV antig Aar25860 HCV polyp Aaw41738 Hepatitis Aav2582 HK7. 9/20 Aav2562 HK7. 9/20 Aay14354 Hepatitis Aay1435806 HCV strai Ad18158 Hepatitis Aar82696 HCV parti Aar82696 HCV parti Aar82696 HCV partis Aar68622 HCV porte Aar6862 HCV portis Aar6862 HCV portis Aar6863 Hepatitis Aar6863 Hepatitis Ad789593 Hepatitis Ad036713 Hepatitis Ad036713 Hepatitis Ad036713 Hepatitis Ad01931 HCV NS4A- Aao18001 Hepatitis Aae15729 Hepatitis Aae15720 Hepatitis
SUMMARIES	AAR22736 AAR22860 AAW1738 AAW26160 AAY1838 AAY1838 AAY1806 AAY1806 AAY1806 AAR82696 AAR82693 AAR82696 AAR82693 AAR82696 AAR82693 AAR82694 AAR836997 AAB31696 AAR831696 AAR816993 AAR17893 AAC18011 AAE15729 AAE15729 AAE15731
DB	UUUUUUULUUUUL 4 4 8 8 8 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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AAB15727 AAB15728 AAB15728 AAB15730 AAB15730 AB057865 AB0578661 AB030581 AB030581 AB030581 AB030582 AB030582 AB030582 AB030582 AB030582 AB030583 AB030583 AB030589	ALIGNMENTS	211 AA.				igen, diagnosi				7.	7.			reagent for antigen pol	Japanese.	ion reacti polypeptid ide contai		Score 525.5; Pred. No. 1. 0; Mismatche	F.	FYGKAIPIEAIKGG	YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT
5.6 5.6 5.6 5.6 6.9 6.6 6.0 6.0 6.0 6.0 6.0 6.0 6.0		tandard; protein;		(first entry)		virus; HCV; ant				92JP-0025002	92JP-0025002	AMA SODA KK.	280/20. 689.	agglutination patitis C virus	age 16-17; 18pp	nological agglutinat uses a HCV antigen igen active polypept	AA;	98.0%; larity 99.0%; Conservative	PHPNIEEVALSNTGEIP	PHPNIEEVALSNTGEIP	LDVSVIPTSGD-VV
5		1 36 AR52736 8	AAR52736;	31-JAN-1995	HCV antigen.	Hepatitis C v	Synthetic.	JP06102273-A.	15-APR-1994.	18-SEP-1992;	18-SEP-1992;	(TOKU ) TOKUYAMA	WPI; 1994-161: N-PSDB; AAQ62	Immunological accomprising hepat	Claim 2-3; Pa	An new immunol hepatitis C us The HCV antige in AARS2735-38	Sequence 211	Query Match Best Local Simil Matches 102; C	1 урнр	зе урна	61 YYRG
U U U U U U U U U U U U U U U U U U U		RESULT AAR527 ID A	X ¥ X	i i	<b>2</b> 图 2	ž Š.	× 8	X & :	X 유	X & I	X & .	X &	<b>X</b>	4 E E	X & :	\$8888	X S	Our Ber Mat	ò	qq	ò

AAR25860

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Hepatitis C virus antigen expressed as recombinant in E.coli - useful for diagnosis of hepatitis C virus infection.
                                                                                                                                                                                                                                                                                                                                      Protein contg. non-A non-B hepatitis antigen fragment - prepd. by culturing transformants transformed by vector contg. base sequence coding specified aminoacid sequences, used for detecting hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 VPHPNIEEVALSNTGEIPPYGKAIPIEAIKGGRHLIPCHSKKKCDELAAKLTGLGLNAVA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VPHPNIEBVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a non-A non-B hepatitis virus (NANBH) or hepatitis C virus (HCV) antigen, useful for diagnosis or detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.0%; Score 525.5; DB 2; Length 226; 99.0%; Pred. No. 1.2e-57; ive 0; Mismatches 0; Indels 1;
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/note= "Sequence AAR25860"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 4; 53pp; Japanese
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(first entry)
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N-PSDB; AAQ27009.
                                                                                                                                                                                                 (SHIM/) SHIMOTONO K. (GREC ) GREEN CROSS
                                                                                                                                                                                                                                                                                       WPI; 1993-260858/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP04179482-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C '
Unidentified
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                                                                                     18-DEC-1991;
                                                                                                                                               18-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1992
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21-JAN-1993
                                20-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR25882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences given in AAR25854-74 are hepatitis C virus protiens. The genes encoding these proteins can each be used to prepare recombinant vectors by ligating the gene of interest in to a vector to be expressed in E. coli. These polypeptides are useful as diagnostic reagents for type C hepatitis and they may be produced efficiently by recombinant methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus antigen expressed as recombinant in E.coli - useful for diagnosis of hepatitis C virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 VPHPNIEEVALSNIGEIPFYGKAIPIEAIKGGRHLIPCHSKKKCDELAAKLTGLGLNAVA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VPHPNIEBVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-A non-B hepatitis virus; NANBH; hepatitis C virus; HCV; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant vector; E. coli; diagnostic; reagent; type C hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.0%; Score 525.5; DB 2; Length 226; Best Local Similarity 99.0%; Pred. No. 1.2e-57; Matches 102; Conservative 0; Mismatches 0; Indels 1.
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61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
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                                                                                                                                                                             226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 3; 66pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90JP-00304417.
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                                                                                                                                                                             AAR25860 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TOKU ) TOKUYAMA SODA KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-263663/32.
                                                                                                                                                                                                                                                                                                                                              HCV polypeptide 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ26987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 226 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP05176774-A.
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                                                                                                                                                                                                                                                                                          21-JAN-1993
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                                                                                                                                                                                                                                     AAR25860;
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Neutralized antibody partial peptide derived from hepatitis C virus - useful for inhibiting Hepatitis C Virus (HCV) serine protease activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the amino acid sequence of a Ser/Thr protease from hepatitis C virus. The invention relates to the use of partial peptides (AAY14348-Y14353) from the anti-HCV neutralising MAb 8D4 for inhibiting HCV serine protease activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
VPHPNIEEVALSNTGEI PFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                                                                                                                                                                                                        Complementarity determining region; CDR; monoclonal antibody; MAb; hepatitis C virus; HCV; protease.
                                                                                           391 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                      Hepatitis C virus Ser/Thr protease amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 525.5; DB 2;
Pred. No. 4.8e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCV strain J antigen sequence.
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99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 102; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP11127861-A
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                                                                                                                                                                                                                                                AAY14354;
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                                                                                                                                                                                       AAY15806
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                                                                                                                                                                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the NS3 region of the hepatitis C virus (HCV) serine protease. The fragment of this sequence represented in AAW26159 is recognised by the monoclonal antibody of the invention. The monoclonal antibody belongs to the IgG class of antibodies. The antibody is produced by fusion cells formed between immunocytes from a HCV infected mammal, and myeloma cells from the same mammal. The antibody is used for diagnosis of HCV infection. As this monoclonal antibody can bind to a certain chain in serine protease and inhibits the enzyme specifically, it can also be used as an agent for neutralising the activity of serine
The sequences given in AAR25876-95 are encoded by the claimed hepatitis C virus genes of the invention which have been inserted into an E. coli vector. These polypeptides are useful as diagnostic reagents for type C hepatitis and they may be produced efficiently by recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease; NS3 region; HCV; hepatitis C virus; monoclonal antibody; 1gG; immunocyte; myeloma cell; inhibitor; neutralising agent.
                                                                                                                                                                                                                                                                                         62 VPHPNIEBVALSNIGEIPFYGKAIPIBAIKGGRHLIFCHSKKKCDELAAKLIGLGLNAVA 121
                                                                                                                                                                                                                                                                  1 VPHPNIEEVALSNIGEIPPYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal antibody against hepatitis C virus serine protease - useful
for diagnosis of HCV infection.
                                                                                                                 Revised record issued on 09-SEP-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                         Length 252;
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Pred. No. 4.8e-57;
0; Mismatches 0;
                                                                                                                                                                                         Score 525.5; DB 2;
Pred. No. 1.4e-57;
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                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW26160 standard; peptide; 631 AA
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Best Local Similarity 99.0%;
Matches 102; Conservative
                                                                                                                                                                                       98.0%;
99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine protease NS3 region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                Matches 102; Conservative
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                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
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                                                                                                                                                        Sequence 252 AA;
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Length 631; Indels us-09-758-308-2.rag

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92JP-00022657
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Best Local Similarity 99.0
Matches 102; Conservative
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identification; cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus; Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV partial proteinase.
                                                                                                                                                                                                                                                                                                                       present invention
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                 cell or tissue
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11-NOV-1996
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ID AAR6
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                                                                                                                                                                                                                                                                                                                                                     331 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 390
                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                          New antigen peptide from hepatitis C virus - useful in examination agent for antibody.
                                                                                                                                                                                                              The specification describes an antigen peptide derived from hepatitis C virus (HCV), which comprises a chain peptide of at least 12 amino acid residues. The peptide chain comprises at least one amino acid sequence selected from Gly Trp Pro or AAV15/64-66. The peptide is useful in methods to detect antibodies directed against HCV. The present sequence
                                                                                                                                                                                                                                                                                                                                          VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                                                                                                                                                                       Gaps
Antigen peptide; HCV J strain; chain peptide; detection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric protein; signal protein; trafficking signal targeting; proteolytic cleavage site; protease; protease inhibitor; enzyme
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                                                                                                                                                                                                                                                                                                   Length 631;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                          391 YYRGLDVSVIPTSGDVVVVAIDALMTGFTGDFDSVIDCNTCVT 433
                                                                                                                                                                                                                                                                                                                                                                              61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS3 protease protein SEQ ID NO:78.
                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                         98.0%; Score 525.5; DB 2
Best Local Similarity 99.0%; Pred. No. 4.8e-57;
Matches 102; Conservative 0: Mirrari
                                                                                                                                                                                            Disclosure; Page 10-13; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADL18158 standard; protein; 631 AA
                                                                                                                                                                                                                                                              represents a HCV strain J antigen
                                                                          97JP-00290165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-AUG-2002; 2002WO-KR001515
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                                                                                             97JP-00290165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kim DH, Lee YJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                 (NIHA ) JAPAN ENERGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-256596/25.
N-PSDB; ADL18157.
                                                                                                                                    WPI; 1999-341639/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                  Hepatitis C virus
                                                                                                                                             N-PSDB; AAX59785
                                                                                                                                                                                                                                                                                 Sequence 631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003014381-A1
                                     JP11124398-A
                                                                          22-OCT-1997;
                                                                                            22-OCT-1997;
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                                                       11-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADL18158;
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ADL18158
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The present invention describes a chimeric protein comprising at least one signal protein that has a trafficking signal targeting to a subcellular organielle and at least one proteolytic cleavage site for a proteolytic standard and at least one proteolytic cleavage site for a proteolytic site or a signal masking protein through the proteolytic site or a signal masking protein through the proteolytic site or a signal masking protein through the proteolytic site or a signal masking protein through the proteolytic site or a signal protein spresent in cytosol; (b) the trafficking signal of at least one signal protein is activated when the proteolytic cleavage site is cleaved to signal protein as a result at least one fragment protein that includes the activated signal protein is labelled with at least one cludes the activated signal protein is labelled with at least one fluorescent protein and the position and intensity distribution of the fluorescent label signal in the cell is altered depending on the cleavage by the protease. Also described: (1) a recombinant gene comprising a nucleic acid sequence encoding the chimeric protein which is constructed to express the chimeric protein in a cell; (2) a cell transformed with the recombinant gene or vector; (3) analysing the activity of a protease inside a cell; (6) a nucleic acid comprising the chimeric protein for detecting protease activity in a cell; (7) a vector comprising the nucleic acid; (8) a kit for detecting a protease inside a cell; (6) a nucleic acid; (8) a kit for detecting a protease inside a cell; (9) a recent or the vector; (1) or protease activity and (1) detecting a protease inside a cell; (1) a vector comprising the nucleic acid; (1) detecting a nucleic acid; (1) detecting a protease inside a cell; (2) a protease includes the chimeric protein for detecting protease includes a protease activity of a protease includes a protease activity of a protease activity and the chimeric protein for detecting protease activity and the chimeric protein in the cell
chimeric protein, useful for detecting protease inhibitors inside the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (9) detecting a protease inside a cell or tissue, and (10) detecting a protease inhibitor in vivo. The chimeric protein is useful for detecting protease inhibitors inside the cell or tissue. The present sequence represents HCV NS3 protease, which is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
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Pred. No. 4.8e-57;
0; Mismatches 0; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YYRGLDVSVIPTSGDVVVVVATDALMTGFTGDFDSVIDCNTCVT 433
                                                                                                                                                                                 Disclosure; SEQ ID NO 78; 214pp; English.
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(first entry)
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Gaps

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This protein from HCV (hepatitis C virus) (encoded by AAQ80498) is cleaved between amino acids 2419 and 2420, by a new serine protease, contg. the sequence of AAR68621. The proteinses is purified as a fused product with the dihydrofolate reductase protein by using a methotrexate column. It can be used for the development of an inhibitor for HCV proteinase. (Updated on 16-OCT-2003 to standardise OS field)
     The present sequence (contg. AAR82693) is that of a partial proteinase isolated from Hepatitis C virus (HCV). The proteinase can be used as an anti-HCV agent. It can also be used to screen cpds. for their ability to inhibit its proteolytic activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New HCV-originated proteinase active substance - used for site-specific cleavage by an intermolecular reaction and the purification thereof.
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                                                                                                                                                         Length 923;
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                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                    YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                                                                                                                                                                             428 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 470
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2419. .2420
/note= "Serine protease cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteinase; serine; cleavage; hepatitis C virus; HCV
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Pred. No. 3.8e-56;
0; Mismatches 0;
                                                                                                                                                       98.0%; Score 525.5; DB 2;
99.0%; Pred. No. 7.9e-57;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serine proteinase
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KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR68622 standard; protein; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCV protein cleavable with new
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Best Local Similarity 99.0
Matches 102; Conservative
                                                                                                                                                                                              Matches 102; Conservative
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(SOYA-) SOYAKU GIJUTSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
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                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3010 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ80498.
                                                                                                                        Sequence 923 AA;
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Cleavage-site
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16-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 425
                                                                                                                                                                                                                                                                                           agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An HCV proteinase active substance - which has activity as an anti-HCV agent and can be used to screen for proteinase inhibitors.
                                                                                                                                                                               as an anti-HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                                                                                                                    The present sequence is that of a partial proteinase isolated from Hepatitis C virus (HCV). The proteinase can be used as an anti-HCV as It can also be used to screen cpds. for their ability to inhibit its proteclyric activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  98.0%; Score 525.5; DB 2; Length 916; llarity 99.0%; Pred. No. 7.8e-57; Conservative 0; Mismatches 0; Indels 1.
                                                                                                                                                                               activity as
inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                                                               An HCV proteinase active substance - which has agent and can be used to screen for proteinase
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                                                    (KAEN/) KAENNO K.
(SUMQ ) SUMITOMO METAL IND LTD.
(SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOYAKU GLJUTSU KENKYUSHO KK
                                                                                                                                                                                                                                      Claim 3; Page 24-27; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR82696 standard; protein; 923
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SUMITOMO METAL IND LTD.
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92JP-00325303.
92JP-00249240.
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(first entry)
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N-PSDB; AAT03959.
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es 102; Conserv
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 18-SEP-1992;
04-DEC-1992;
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04-DEC-1992;
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14-NOV-1996
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AAR82696;

RESULT 10

(KAEN/) (SUMO)

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Query Match

Best Loca Matches

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Gaps

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92JP-00249241.
                                                   N-PSDB; AAQ81559.
                                                                                                                                         Sequence 3010 AA;
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18-SEP-1992;
              18-SEP-1992;
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14-NOV-1996
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       9
       1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                Hepatitis C virus; HCV; non-A non-B; helicase gene; RNA helicase; baculovirus; recombinant production.
                                   2240. .2242
/label= N-linked glycosylation site
2788. .2790
/label= N-linked glycosylation site
                                                                                                                                                                                            196. .198
/label= N-linked glycosylation site
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/label= N-linked glycosylation site
250. 252
/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation
                                                                                       AAR68864 standard; protein; 3010 AA
                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                   Hepatitis C virus RNA helicase.
                                                                                                                                                                                                                                                                                                423. .425
/label= N-
                                                                                                                                                                                                                                                                                                                                           532. .534
/label= N-
                                                                                                                                                                                                                                                                                                              430. .432
/label= N-
                                                                                                                    (first entry)
                                                                                                                                                                       Hepatitis C virus
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                                                                                                                     06-DEC-1995
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1357 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                          AAQ81559 encodes AAR68864 hepatitis C virus (HCV) RNA helicase. The DNA was used in the construction of an expression vector, which was used to transform a baculovirus host. The transformed baculovirus could then be used for the recombinant prodn. of HCV RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                                                                                                                                                            of hepatitis C virus helicase gene in baculovirus - useful for large scale prodn. of RNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteinase; hepatitis C virus; screening; inhibitor; proteolytic; identification; cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.0%; Score 525.5; DB 2; Length 3010; 99.0%; Pred. No. 3.8e-56; ive 0; Mismatches 0; Indels 1;
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898. .1233
Thote= "partial proteinase; see AAR82692"
992. .1907
/note= "partial proteinase; see AAR82693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partial HCV non-structural polyprotein.
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(SUMQ ) SUMITOMO METAL IND LTD.
(SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                    졌
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR82694 standard; protein; 3010 AA
                                                    (SOYA-) SOYAKU GIJUTSU KENKYUSHO
                                                                                                                                                                                                                                                                 Claim 1; Fig 1-4; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-00018854.
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92JP-00249241
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.0 Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus, Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-287962/38.
N-PSDB; AAT03960.
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                                                                                                                                                                      The present sequence is a partial Hepatitis C Virus (HCV) polyprotein from the non-structral region. Partial proteinase sequences (AAR82692-93) are contained within this sequence. The proteinases can be used as anti-HCV agents. They can also be used to screen cpds. for their ability to inhibit their proteolytic activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)
An HCV proteinase active substance - which has activity as an anti-HCV agent and can be used to screen for proteinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.0%; Score 525.5; DB 2; Length 3010; Best Local Similarity 99.0%; Pred. No. 3.8e-56; Matches 102; Conservative 0; Mismatches 0; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver cancer; hepatitis-C virus; NS3 gene; carcinogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1417 YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 6; 36pp; Japanese
                                                                                                        Disclosure; Page 39-48; 52pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF88597 standard; protein; 3010 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3010 AA;
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Sequence 3010 AA;

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1357 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an antigenic epitope from a hepatitis C virus (HCV) NS3 protein. The peptide comprises amino acids 1471-1573 of the HCV polyprotein. The specification describes antigenic epitopes from HCV core protein, NS3 protein, NS4 protein and NS4 protein and NS4 protein and HCV in a biological sample. They are also useful for monitoring HCV in a patient sample in addition to diagnostic reagents for detecting HCV in a patient sample in addition to diagnosis. Pharmaceutical compositions comprising the peptides are useful for preventing, minimizing or reducing HCV infection in patients who have been exposed to HCV or to individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New (mosaic) polypeptides, useful as reagents in assays for the diagnosis or monitoring of HCV infections and as components of anti-HCV vaccines, comprises antigenic groups of hepatitis C virus (HCV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      such as health care workers or blood product recipients, who are more likely to become exposed to HCV infection. The antigenic peptides are also useful for generating antibodies which can be used to detect HCV proteins in a sample or for laboratory research purposes
                                                            1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                      Jen; HCV; polyprotein; core protein; NS3 protein; NS4 protein; protein; HCV infection.
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 Length 3010;
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                                                                                                                                                                                                                                                                                                                                         Antigenic epitope of the Hepatitis C virus (HCV) NS3 protein.
                                                                                                                                               YYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVT 1459
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                                 Indels
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Pred. No. 1.4e-57;
0; Mismatches 0;
                                 ö
Score 525.5; DB 7
Pred. No. 3.8e-56;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                                                                                                             AAB31696 standard; peptide; 101
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98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US015578
                                                                                                                                                                                                                                                                                                           30-APR-2001 (first entry)
     Query Match
Best Local Similarity 99.0
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Khudyakov YE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-138316/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fields HA,
                                                                                                                                                             1417
                                                                                                                                                                                                                                                                             AAB31696;
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                                                                                                                                                                                                                                                                                                                                                                            Antigen;
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61 YYRGLDVSVIPTSGDVVVATDALMYGFTGDFDSVIDCNTCVT 102 *장* 원

Search completed: August 12, 2005, 14:14:58 Job time : 109.012 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2005, 14:04:54 ; Search time 28.57 Seconds (without alignments) 266.510 Million cell updates/sec Run on:

536 1 VPHPNIEEVALSNTGEIPFY......LMTGFTGDFDSVIDCNTCVT 102 US-09-758-308-2 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:\* Database :

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/BCOWB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	αI	Description
-	525.5	98.0	278	4	US-08-635-886C-268	Sequence 268, App
8	525.5	98.0	278	4	US-08-974-690C-268	268,
m	514.5	96.0		4	US-08-635-886C-272	272,
4	514.5	96.0	278	4	US-08-974-690C-272	272,
S	513.5	95.8		m	US-09-198-723A-69	69
9	513.5	95.8	646	4	US-09-684-881-69	69
7	512.5	95.6	278	4	US-08-635-886C-273	273,
89	512.5	95.6	278	ぜ	US-08-974-690C-273	273,
Q	512.5	95.6	1985	4	US-09-539-601-9	9, A
10	512.5	95.6	1985	4	US-09-539-601-12	12,
11	512.5	95.6	1985	4	US-09-539-601-24	24,
12	512.5	95.6	1985	4	US-09-539-601-30	30,
13	512.5	92.6	2201	4	US-09-539-601-6	Sequence 6, Appli
14	512.5	95.6	2201	4	US-09-539-601-15	15,
15	512.5	92.6	2201	4	US-10-029-907-3	'n
16	512.5	92.6		4	US-09-539-601-3	3, 1
17	512.5	92.6	3010	4	US-09-539-601-27	27,
18	512.5	92.6	3010	4	US-09-539-601-33	33,
19	508.5	94.9		4	US-08-635-886C-271	271,
50	508.5	94.9		4	US-08-974-690C-271	271,
21	507.5	94.7	278	4	US-08-635-886C-274	274,
22	507.5	94.7		4	US-08-974-690C-274	274,
23	507.5	94.7	609	7	US-08-324-977-40	40, 7
24	507.5	94.7	609	~	US-08-384-616-40	40
25	507.5	94.7	609	~	US-08-904-686A-40	40
56	507.5	94.7	609	m	US-09-315-850-40	Sequence 40, Appl
27	507.5	94.7	631	-	US-08-700-356-1	Sequence 1, Appli

Sequence 1, Appli sequence 23, Appl sequence 20, Appl sequence 60, Appl sequence 61, Appl sequence 61, Appl sequence 61, Appl sequence 61, Appl sequence 11, Appli se	
US-08-936-865-1 US-09-198-723A-23 US-09-684-881-23 US-09-198-723A-66 US-09-198-723A-66 US-09-198-723A-66 US-09-198-723A-66 US-09-684-881-60 US-09-684-881-66 US-09-684-881-66 US-09-684-881-66 US-09-684-881-66 US-09-684-881-66 US-09-684-81-72 US-09-543-376B-2 US-09-543-376B-3 US-09-198-723A-13 US-09-198-723A-13	
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# ALIGNMENTS

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Sequence 268, Application US/08635886C

Sequence 268, Application US/08635886C

Patent No. 6555114

GENERAL INPORMATION:

APPLICANT: LEROUX-ROELS, Geert

APPLICANT: DELEYS, Robert

TITLE OF INVENTION: MARKTENS, Geert

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 275-18

CURRENT APPLICATION NUMBER: US/08/635,886C

CURRENT FILING DATE: 1996-04-25

PRIOR APPLICATION NUMBER: EP 93402718.6

PRIOR FILING DATE: 1994-10-28

PRIOR FILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOCTWARE PATENCATION NUMBER: EP 93402718.6

SOCTWARE PATENCATION NUMBER: DE 93402718.6
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Sequence 268, Application US/08974690C

Patent No. 661333

GENERAL INFORMATION:

APPLICANT: LEROUX-ROELS, Geert

APPLICANT: DESCUINANT: MARTENS, Geert

TITLE OF INVENTION: UNRONOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C

TITLE OF INVENTION: VIRUS

TITLE OF INVENTION: VIRUS

FILE REFERENCE: 2251-94

CURRENT APPLICATION NUMBER: US/08/974,690C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
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CRGANISM: hepatitis C virus
US-08-635-886C-268
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Best Local Similarity 99.04
Matches 102; Conservative
US-08-635-886C-268
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US-09-198-723A-69
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                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                  1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 60
                                                                                                                                                                                                                                                                  1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA 60
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US-08-974-690C-272
; Sequence 272, Application US/08974690C
; Patent No. 661333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROBLS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MARRIENS, Geert
; APPLICANT: MARRIENS, Geert
; TILLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
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Pred. No. 6.2e-57;
4; Mismatches 0; Indels 1
                                                                                                                                                                                                       Length 278;
                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                     Query Match 98.0%; Score 525.5; DB 4; Best Local Similarity 99.0%; Pred. No. 2.5e-58; Matches 102; Conservative 0; Mismatches 0;
CURRENT FILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR FILING DATE: 1994-10-28
PRIOR PPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: Patentin version 3.1
LENGTH: 278
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95.1%;
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ORGANISM: hepatitis C virus
                                                                                                                                          ; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-268
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Best Local Similarity 95.13
Matches 98, Conservative
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US-08-635-886C-272
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1 VPHPNIEEVALSNTGEIPFYGKAIPIEAIKGGRHLIFCHSKKKCDELAAKLTGLGLNAVA
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APPLICANT: Taremi, Shahriar S.
APPLICANT: Taremi, Shahriar S.
APPLICANT: Weber, Patricia
APPLICANT: Weber, Patricia
APPLICANT: Weber, Patricia
TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus
TITLE OF INVENTION: NS3 Protease and NS4A Cofactor Peptide
NUMBER OF SEQUENCES:
ADDRESSEE: Schering-Plough Corp.
STREET: 2000 Galloping Hill Road
CITY: Kenilworth
STRATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                             Score 514.5; DB 4; Length 278;
Pred. No. 6.2e-57;
4; Mismatches 0; Indels 1;
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FILLE OF INVENTION: VIRUS
FILE REFERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT FILING DATE: 1997-11-19
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR APPLICATION NUMBER: EP 93402718.6
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SEQ ID NO 272
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MEDIUM TYPE: Floppy disk
COMPUTER: Power Macintosh
OPERATING SYSTEM: 8.0.1
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/198,723A
PILLING DATE: 24 NOV 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 69, Application US/09198723A; Patent No. 6211338; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AMME: MCLBUGhlin, Jaye P.
REGISTRATION NUMBER: 41,211
REPRENCK/DOCKET NUMBER: JBOG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)298.5056
                                                                                                                                                                                                                                                                                                                                                                                                                  96.0%;
95.1%;
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TELEPAX: (908)298-5388
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: hepatitis C virus US-08-974-690C-272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98; Conservative
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Best Local Similarity
Matches 98; Conserv
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US-08-974-690C-273
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US-08-635-886C-273
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                    Gaps
                                                                                                                                                                                                                                                                                                     APPLICANT: Malcolm, Bruce
Taremi, Shahriar S.
Wabor, Patricia
Yao, Nanhua
TITLE OF INVENTION: Covalent Complexes of Hepatitis C Virus
NUMBER OF SEQUENCES: 123
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                  0; Indels
                                                                                                                        61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT 102
                                                                                                                                           406 YYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVT 448
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Pred. No. 2.5e-56;
4; Mismatches 0
   95.1%; Pred. No. 2.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Power Macinican
COMPUTER: Power Macinican
OPERATING SYSTEM: 8.0.1
SOFTHARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/684,881
FILING DATE: 06-0ct-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/198,723
FILING DATE: 24 NOV 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MCLAUGhlin, Jaye P.
REGISTRATION NUMBER: 41.211
REFERENCE/DOCKET NUMBER: JB0800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-5056
TELEFRA: (908) 298-5388
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corp.
STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
                                                                                                                                                                                                                                              Sequence 69, Application US/09684881
Patent No. 6653127
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 646 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     uuery Match
Best Local Similarity 95.1%;
Matches 98; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Kenilworth
                  98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07030
Best Local Similarity
Matches 98; Conserv
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RESULT

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sequence 273, Application US/08974690C

sequence 273, Application US/08974690C

patent No. 661333

sequence 273, Application US/08974690C

patent No. 6613333

sequence 273, Application US/08974690C

patent No. 6613333

sequence 273, Application Select

papelicant: DERGOMA-ROBLS, Geert

papelicant: DERGOMA-ROBLS, Geert

papelicant: DAGRETS, Geert

papelicant: DAGRETS, Geert

price of invention: Invuloominant Human T Cell Epitopes OF Hepatitis C

TITLE OF INVENTION: UNBUSE: US/08/974,690C

CURRENT APPLICATION NUMBER: US/08/974,690C

CURRENT FILING DATE: 1997-11-19

price papelication NUMBER: EP 93402718.6

price papelication NUMBER: EP 93402718.6

price papelication NUMBER: EP 93402718.6

price papelication NUMBER: 286

price papelication NUMBER: 286

price papelication version 3.1

price papelication version 3.1

price papelication version 3.1
Sequence 273, Application US/08635886C

Sequence 273, Application US/08635886C

Patent No. 655514

GENERAL INPORMATION:
APPLICANT: LERGOUX-POELS, Geert
APPLICANT: DELEXOX-POELS, Geert
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C.
TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C.
TITLE OF INVENTION: IMMUNOBER: US/08/635,886C

CURRENT FILING DATE: 1994-0.28

PRIOR PILING DATE: 1994-10-28

PRIOR FILING DATE: 1994-10-28

PRIOR FILING DATE: 1993-11-04

NUMBER OF SEQ ID NOS: 286

SOFTWARE: Patentin version 3.1

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Pred. No. 1.1e-56;
3; Mismatches 1;
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Pred. No. 1.1e-56;
3; Mismatches 1
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OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (60)...(60)
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.6%;
95.1%;
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Local Similarity 95.1%;
les 98; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: hepatitis C virus
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Best Local Similarity 95.1
Matches 98; Conservative
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392 YYRGLDVSVIPTSGDVIVVATDALMTGFTGDFDSVIDCNTCVT 434
                                                          RESULT 11
US-09-539-601-24
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1985
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US-09-539-601-30
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US-09-539-601-6
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                                        170 VPHPNIEEVALSNTGEIPFYGKAIPIEVIKGGRHLIFCHSKKKCDELAAKLSGLGINAVA 229
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95.6%; Score 512.5; DB 4; Length 1985;
Best Local Similarity 96.1%; Pred. No. 1.4e-55;
Matches 99; Conservative 2; Mismatches 1; Indels 1;
                                                                                                                                                                                                                                         Sequence 9, Application US/09539601C

Batent No. 6630343
GENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW
TILE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SEQ ID NOS: 51
SEQ ID NOS: 51
SEQ ID NOS: 51
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US-09-539-601-12

Sequence 12, Application US/09539601C

Patent No. 6610343

GENERAL INFORMATION:

APPLICANT: Bartenschlager, Ralf FW

TITLE OF INVENTION:

PILE REFERENCE: all sequences

CURRENT FPLICATION NUMBER: US/09/539,601C

CURRENT FPLICATION NUMBER: 199 15 178.4 GERMANY

EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY

MUMBER OF SEQ ID NOS: 51

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 12.
                                                                                                                          230 YYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YYRGLDVSVIPTSGDV-VVATDALMTGFTGPFDSVIDCNTCVT 102
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                                                                                                     61 YYRGLDVSVIPTSGD-VVVATDALMTGFTGDFDSVIDCNTCVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-539-601-9
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; ORGANISM: Hepatitis C virus
US-09-539-601-12
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332 VPHPNIEEVALSSTGEIPFYGKAIPIETIKGGRHLIFCHSKKKCDELAAKLSGLGLNAVA 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System;
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 1985
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                                                                           APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REPERRNCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
Sequence 24, Application US/09539601C; Patent No. 6630343; GENERAL INFORMATION:
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; Patent No. 6630343
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Best Local Similarity 96.1%;
Matches 99; Conservative 2
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TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REPERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver. 2.1
SQT DN 0 15
LENGTH: 2201
TYPE: PRT
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APPLICANT: Barrenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER PILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SEQ ID NOS: 51
SEQ ID NO 6
LENGTH: 2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BOSHRINGER INGELHEIM (CANADA) LTD.
TITLE OF INVENTION: SELF REPLICATING RNA MOLECULE FROM
TITLE OF INVENTION: HEPATITIS C VIRUS
FILE REPERENCE: 13/083
CURRENT APPLICATION NUMBER: US/10/029,907
CURRENT FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                  Query Match 95.6%; Score 512.5; DB 4, Best Local Similarity 96.1%; Pred. No. 1.6e-55; Matches 99; Conservative 2; Mismatches 1.
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Pred. No. 1.6e-55;
2; Mismatches 1
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Patent No. 6706874
GENERAL INFORMATION:
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Best Local Similarity 96.1%;
Matches 99; Conservative ;
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                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-539-601-6
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US-09-539-601-15
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RESULT 1
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501
1 MSTNPKPQRKTKRNTNRRPQ......GRTWAQPGYPWPLYGNEGM 91
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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genescqp1990s: 
genescqp2000s: 
genescqp2001s: 
genescqp2002s: 
genescqp2003ss: 
genescqp2003bs: 
genescqp2004bs:
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

uo	Antigenic	Hepatitis	Recombina	HCV in pl	Hepatitis	Protein #	HCV in pl	Nucleic a	HCV fusio	HCV pepti	Hepatitis	Partial H	Hepatitis	HCV core	Hepatitis	Protein e	Hepatitis	Core prot	HCV core	HCV EN-80	Hepatitis	HCV unpro	Hepatitis	Hepatitis	Mouse pro
Description	Aab31695	Aay82358	Aaw33689	Aar24525	Aar92954	Aab73170	Aar24527	Aaw33691	Aar53921	Aar88311	Aar68864		Adf88597	Aar40978	Aaw30583	Aay01614	Adf66059	Aar35758	Aar56597	Aar54641	Aaw18199	Aaw07484	Aaw33687	Aaw33688	Aaw33695
αi	AAB31695	AAY82358	AAW33689	AAR24525	AAR92954	AAB73170	AAR24527	AAW33691	AAR53921	AAR88311	AAR68864	AAR82694	ADF88597	AAR40978	AAW30583	AAY01614	ADF66059	AAR35758	AAR56597	AAR54641	AAW18199	AAW07484	AAW33687	AAW33688	AAW33695
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.4	99.2	99.2	99.2
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AAR92955 AAR92953 AAW33690	AAW68461 AAW68465 AAW68466 ABB77253	AAB18537 ABB77254 ADN35970 ADL16316	ADF08480 AAY14970 ADN33109 AAR92947	AAE19889 ABW00340 AAR44010 AAW41754 AAR92938
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26 27 28	32 32 32 32	333	338 388 40	4 4 4 4 12 6 4 4 6 15 4 6 7

### ALIGNMENTS

AAB31695;	
30-APR-2001 (first entry)	
Antigenic epitope of the Hepa	Antigenic epitope of the Hepatitis C virus (HCV) core protein.
Antigen; HCV; polyprotein; cc NS4a protein; HCV infection.	Antigen; HCV; polyprotein; core protein; NS3 protein; NS4 protein; NS4a protein; HCV infection.
Hepatitis C virus.	
WO200104149-A1.	
18-JAN-2001.	
07-JUL-2000; 2000WO-US018704.	
09-JUL-1999; 99WO-US015578.	
(USSH ) US DEPT HEALTH & HUMAN SERVICES	IN SERVICES.
Fields HA, Khudyakov YE;	
WPI; 2001-138316/14.	
New (mosaic) polypeptides, useful as reagents in assa or monitoring of HCV infections and as components of comprises antigenic groups of hepatitis C virus (HCV)	New (mosaic) polypeptides, useful as reagents in assays for the diagnosis or monitoring of HCV infections and as components of anti-HCV vaccines, comprises antigenic groups of hepatitis C virus (HCV).
Claim 2; Page 39; 52pp; English.	sh.
The present sequence represer	The present sequence represents an antigenic epitope from a hepatitis C
virus (HCV) core protein. The	core protein. The peptide comprises amino acids 1-91 of the
HCV polyprotein. The specific	HCV polyprotein. The specification describes antigenic epicopes from heve antigenic and antigenic
core procein, Mss procein, Ms neptides are useful as diagno	core process, was process, was process and was process; and analysis and another are useful as diagnostic readents for detecting HCV in a
biological sample. They are	biological sample. They are also useful for monitoring HCV infection in a
patient sample in addition to	patient sample in addition to diagnosis. Pharmaceutical compositions
comprising the peptides are	comprising the peptides are useful for preventing, minimizing or reducing
HCV infection in parients win	ACV INTECTION IN PARTIEURS WIG TAVE EXPOSED CONTROL OF THE TAVELLEY.
Such as nealth care workers of	BUCH BB HEALTH CARE WOLKELB OF DISCUSTION THE BUTIEFFICES, WILL STEEL TO ALL OF THE STEEL THE BUTIEFFICES. THE BUTIEFFICES THE
also useful for denerating at	ilkely to become exposed to not intection: The untigenty population allowed to detect HCV
proteins in a sample or for	proteins in a sample or for laboratory research purposes

91

RROPI PKARRPEGRTWAQPGYPWPLYGNEGM

61

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an oligonuclectide sequence which potentiates the expression of a useful gene when incorporated in a gene expression vector, where the oligonuclectide sequence consists of the 5'-non-translated region (5'UTR) of a viral genome or its fragment or modified form. The 5'UTR sequence is useful in screening potential initiation factors of interaction with the viral IRES or IRES-dependency, for treatment of diseases caused by cap-dependent mRNA translation and in the diagnosis of the severity of HCV infection. The present sequence represent sequence from a Hepatitis type C virus (HCV) exemplification of the present invention
                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequence which potentiates gene expression and contains 5' non-translated region of a viral genome is incorporated in vectors for improving the expression of a useful gene.
                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; 5' UTR; 5'-nontranslational region; diagnosis; gene expression; infection; IRES; viral.
                                                                         1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                            1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                   Gaps
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                             Length 91;
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                                                  Indels
                                                                                                                                                                                                                                                           Hepatitis type C virus protein sequence SEQ ID NO:1.
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                            / Match 100.0%; Score 501; DB 4; Local Similarity 100.0%; Pred. No. 8.9e-47; Nes 91; Conservative 0; Mismatches 0;
                                                                                                                  91
                                                                                                                              RROPIPKARRPEGRTWAQPGYPWPLYGNEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 82-84; 94pp; Japanese.
                                                                                                                                                                                             AAY82358 standard; protein; 124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                99WO-JP003682
                                                                                                                                                                                                                                                                                                                                                                                                    98JP-00241367
                                                                                                                                                                                                                                                                                                                                                                                                                        (FUSO ) FUSO PHARM IND LTD.
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-237867/20.
                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
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N-PSDB; AAA08097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 124 AA;
         Sequence 91 AA;
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                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                    27-AUG-1998;
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                                                                                                                                                                                                                 AAY82358;
                              Query Match
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Matches
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This is a recombinant protein 120NA. This recombinant protein contains
the Hepatitis C virus (HCV) core polypeptide 120 fused to a nucleic acid-
binding motif present in the HBC protein of Hepatitis B virus (HBV). This
recombinant protein can be bound to a nucleic acid in the host for
producing a nucleic acid-bound polypeptide by a new method. The method
comprises producing a fusion gene containing the polypeptide and the
nucleic acid-binding motif, binding a nucleic acid to the polypeptide as
a soluble fraction, and purifying the nucleic acid-bound polypeptide from
the soluble fraction. When the polypeptide caid-bound polypeptide from
cantigen, the nucleic acid-bound polypeptide is a recombinant form of an
antigen, the nucleic acid-bound polypeptide caid bound polypeptide caid-bound polypeptide can be used as an immunoassay
reagent for detecting the antigen or an antibody to the antigen,
especially in an agglutination assay using particles coated with the
nucleic acid-bound polypeptides can be applied to diagnosis
of disease and infection, especially for the detection of HBV and HCV
polypeptides. The nucleic acid-bound polypeptides may be immunoreactive
in cases where the free polypeptide is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid-binding motif; HCV; HBV; Hepatitis C virus; diagnosis; core polypeptide; immunoassay; detection; antigen; disease; infection; Hepatitis B virus; recombinant.
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100.0%; Pred. No. 1.7e-46;
ive 0; Mismatches 0;
61 RRQPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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                                                                                                                                                                                             AAW33689 standard; protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
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                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant protein 120NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FJRE ) FUJIREBIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Takemura F, Ueno E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-529030/49.
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Hepatitis B virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                    AAW33689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
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1 MSTNPKPORKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG

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DNA and amino acid sequence of HCV envelope 1 and core proteins - used to determine HCV genotype and as vaccines against HCV infection.
                                                                                                                                                                                                                                                                                                                                 AAR92936-R92987 are HCV core proteins derived from 52 different HCV isolates. Isolated cDNA sequences are used for the prodn. of primers useful for detecting the presence of HCV in a sample, the primers are also useful for HCV genotyping. Proteins encoded by the cDNAs can be used in vaccines for immunising against HCV infection. The proteins may also be used to detect antibodies against HCV in serum, saliva, lymphocytes or other mononuclear cells. The antibodies may be used in the prevention of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral infection, RecQ helicase, liver disorder, HCV infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 501; DB 2; Length 1 100.0%; Pred. No. 2e-46; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RRQPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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                                                                                                                                                                                                                                                                                                   Claim 4; Page 195-196; 340pp; English.
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                                                                                                                                                              RH;
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                                                            95WO-US010398
                                                                                          94US-00290665
                                                                                                                                                               Purcell
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                                                                                                                              (USSH ) US SEC DEPT HEALTH.
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(first entry)
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les 91; Conservative
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N-PSDB; AAF63461.
                                                                                                                                                                                               WPI; 1996-139709/14
                                                                                                                                                              Bukh J, Miller RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                   N-PSDB; AAT16628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 191 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               liver cancer.
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                                                              15-AUG-1995;
                                                                                              15-AUG-1994;
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11-MAY-2001
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                              22-FEB-1996.
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Best Local Si
Matches 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in AAR24525-27 are examples of a new structural gene of hepatitis C virus (HCV) encooded by various expression vectors. This polypeptide has HCV antigen activity and can be used to recognise anti-HCV antibodies existing in the serum of HCV patients specifically. It can be used as a diagnostic agent by the agglutination or ELISA method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New structural protein gene of hepatitis C virus - encodes specific sequence of 163 aminoacid(s), useful for the diagnosis of hepatitis C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSTINPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      envelope 1; core protein; HCV genotyping; antibody; vaccine;
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              RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 96
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                                                                                                                                                                                                                                     HCV; antibody; agglutination; ELISA.
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                                                                                                 AAR24525 standard; protein; 191
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                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TOKU ) TOKUYAMA SODA KK
                                                                                                                                                                                                   HCV in plasmid pKMR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SHIM/) SHIMOTONO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-214123/26.
                                                                                                                                                                                                                                                                     Hepatitis C virus.
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                                                                                                                                                                   07-DEC-1992
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hepatitis.
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                                                                                                                                                                                                                                                   9
                                                                            compounds, which
                                                                         The present invention relates to a method for screening compounds, which interfers with the inhibition of the function of RecQ helicases by hepatitis C virus (HCV) proteins. The method can be used to identify compounds which can be used for the prevention and treatment of liver disorders associated with HCV infection, such as liver cancer. The present sequence was used in the present invention. (Updated on 06-AUG-2003 to correct OS field.)
          Screening method for substances interfering with the inhibition of WRN helicase by hepatitis C virus protein for use in preventing liver disorders such as cancer associated with hepatitis C infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New structural protein gene of hepatitis C virus - encodes specific sequence of 163 aminoacid(s), useful for the diagnosis of hepatitis C.
                                                                                                                                                                                                                                           1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                   100.0%; Score 501; DB 4; Length 191; 100.0%; Pred. No. 2e-46; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                              91
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                                                                                                                                                                                                                                                                                       RROPIPKARRPEGRTWAQPGYPWPLYGNEGM
                                                      Disclosure; Page 52-53; 64pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV; antibody; agglutination; ELISA
                                                                                                                                                                                                                                                                                                                                                    AAR24527 standard; protein; 263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 5; 13pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                          91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TOKU ) TOKUYAMA SODA KK. (SHIM/) SHIMOTONO K.
                                                                                                                                                                                                                                                                                                                                                                                                                    HCV in plasmid pNSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-214123/26.
                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
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                                                                                                                                                                Sequence 191 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1992
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                                                                                                                                                                                     Query Match
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Length 263;

Score 501; DB 2; Pred. No. 2.8e-46;

100.0%;

Query Match Best Local Similarity

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This is a nucleic acid-bound polypeptide 120NA120. This contains the Hepatitis C virus (HCV) core polypeptide 120 and a nucleic acid-binding motif present in the HBC protein of Hepatitis B virus (HBV). This nucleic acid-bound polypeptide can be produced by a new method. The method comprises producing a fusion gene containing the polypeptide and the nucleic acid-bound polypeptide as a soluble fraction. When the polypeptide is a recombinant form of an antigen, the nucleic acid-bound polypeptide from antigen, the nucleic acid-bound polypeptide is a recombinant form of an antigen, the nucleic acid-bound polypeptide can be used as an immunoassay reagent for detecting the antigen or an antibody to the antigen, the nucleic acid-bound polypeptide can be used as an immunoassay reagent for detecting the antigen or an antibody to the antigen.

C especially in an agglutination assay using particles coated with the nucleic acid-bound polypeptides. The methods can be applied to diagnosis of disease and infection, especially for the detection of HBV and HCV consequence of the properties of the properties of the methods and the muchoreactive consequence of the muchos of the methods of the
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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                  1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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100.0%; Pred. No. 3e-46;
ative 0; Mismatches 0; Indels
                                                                                                                                                                                        RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
                                                                                                                                                                                                                                                                      91
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                                                                                                                                                                                                                                         Nucleic acid-bound polypeptide 120NA120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW33691 standard; protein; 281
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es 91; Conserv
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Hepatitis C virus.
Hepatitis B virus.
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The HCV envelope proteins defined by amino acids 1-191, 192-383 and 384-980 of sequence AAR53921 are claimed. The proteins have mol.wt. 22, 35 and 70 kD, respectively, and are useful for preparing vaccines against HCV
                                                                                                                                                                                                                                 Protein constituting hepatitis C virus particles and its expression useful for preparation of vaccines.
782. .805
/label= transmembrane_region
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                                                                                                          91JP-00359636.
                                                                                                                                         91JP-00359636
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Best Local Similarity 100..
                                                                                                                                                                                            WPI; 1994-147948/18.
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N-PSDB; AAT03677.
                                                                                                                                                                      (SHIM/) SHIMOTOYA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 980 AA;
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                                            JP06092996-A.
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                                                                                                          28-DEC-1991;
                                                                                                                                         28-DEC-1991;
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                                                                            05-APR-1994.
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 Region
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 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 63
                                                                                                                                                                                                                                                                     Hepatitis C virus; HCV; envelope protein; open reading frame; vaccine.
                                                                                                                                                                                                                                      HCV fusion protein corresp. to N-terminal of ORF.
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//abel= N-glycosylation_site
430. 432
//abel= N-glycosylation_site
448. 450
//abel= N-glycosylation_site
540. 542
//abel= N-glycosylation_site
556. 558
//abel= N-glycosylation_site
576. 578
//abel= N-glycosylation_site
645. 647
//abel= N-glycosylation_site
645. 647
//abel= N-glycosylation_site
645. 647
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/label= transmembrane_region
718. .727
/label= transmembrane_region
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label= N-glycosylation site
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label= N-glycosylation_site
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|abel= N-glycosylation_site
                               RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
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/label= signal_sequence
191...192
192...383
/label= gp35
/note= "Claim 1"
                                                 64 RROPIPKARRPEGRTWAQPGYPWPLYGNEGM
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                                                                                                                                            AAR53921 standard; protein; 980 AA.
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/label= gp70/p19
/note= "Claim 2"
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/label= p22
/note= "Claim 3"
174. .191
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                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
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Protein
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                                61
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Protein
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                                                                                                             RESULT 9
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Length 980;

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                                                                                                        1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                        Gaps
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0
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                                                     0; Indels
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100.0%; Score 501; DB 2;
100.0%; Pred. No. 1.2e-45;
ive 0; Mismatches 0;
                                                                                                                                                                                                               61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
                                                                                                                                                                                                                                               61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
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25-JUL-1995.
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      This sequence is encoded by a fragment of the hepatitis C virus (HCV) genome including the hypervariable region. The DNA region is amplified by the primer sequences given in AAT03664-73. The amplified product is subjected to electrophoresis under denaturing conditions. The primers may be used in combination with the primer sequences given in AAT03674-76. Preferably, primer MS1, MS2, MS3, MS4, MS5 or MS6 and an oligo selected from MR1, MR2 or MR1, are used as primer pairs
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                                                                                                                                              1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; non-A non-B; helicase gene; RNA helicase; baculovirus; recombinant production.
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                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-45;
Matches 91; Conservative 0; Mismatches 0; Indels 0;
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/label= N-linked glycosylation site
1213. .1215
/label= N-linked glycosylation site
1255. .1257
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|abel= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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'label= N-linked glycosylation site
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/label= N-linked glycosylation site
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|Jabel= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation
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/label= N-linked glycosylation
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/label= N-linked glycosylation
                                                                                                                                                                       RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
                                                                                                                                                                                         RROPI PKARRPEGRTWAQPGYPWPLYGNEGM 91
                                                                                                                                                                                                                                      AAR68864 standard; protein; 3010 AA
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                         Hepatitis C virus RNA helicase.
                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus.
                                                                                 Sequence 1010 AA;
                                                                                                                                                                                                                                                                         06-DEC-1995
                                                                                                                                                                                                                                                       AAR68864;
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                                                                                                                                                                                                                              AAR68864
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AAQB1559 encodes AAR68864 hepatitis C virus (HCV) RNA helicase. The DNA was used in the construction of an expression vector, which was used to transform a baculovirus host. The transformed baculovirus could then be used for the recombinant prodn. of HCV RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSTNPKPORKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of hepatitis C virus helicase gene in baculovirus - useful for large scale prodn. of RNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteinase; hepatitis C virus; screening; inhibitor; proteolytic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 501; DB 2; Length 3010; 100.0%; Pred. No. 3.8e-45; ive 0; Mismatches 0; Indels 0;
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Thotes "Bartial proteinase; see AAR82692"
992. .1907
/note= "partial proteinase; see AAR82693"
'label= N-linked glycosylation site
                    2041. .2043
/label= N-linked glycosylation site
                                                                                                                                                2788. .2790
/label= N-linked glycosylation site
                                                                                   2240. .2242 ------ signal on /label = N-linked glycosylation 2788. .2790
                                                            2077. .2079
/label= N-linked glycosylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partial HCV non-structural polyprotein.
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                                                                                                                                                                                                                                                                                                                                                                                             (SOYA-) SOYAKU GIJUTSU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR82694 standard; protein; 3010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 1-4; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                       92JP-00249241.
                                                                                                                                                                                                                                                                                                                                                  92JP-00249241.
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Best Local Similarity 100.0
".rches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification; cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; Virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-040330/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ81559.
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                                                                                                                                                                                                                      JP06319583-A.
                                                                                                                                                                                                                                                                                                         18-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                    18-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2003
14-NOV-1996
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This sequence represents the N-terminal 97 amino acids of the hepatitis C virus (HCV) core protein. Peptide fragments derived from this sequence contained epitopic regions. These peptides may be used alone or as a part of a larger peptide, or in a mixture of peptides for the detection of HCV or in a vaccine for its prevention. See also ARR40979-99. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS
      The invention relates to the novel testing method for diagnosing liver cancer. The novel method comprises amplifying the amino terminal region of a hepatitis-C virus NS3 gene using a predatermined primer and determining the hepatitis-C virus in a base sequence of the obtained but fragment. The novel testing method is useful for diagnosing liver cancer and also used in a gene amplification technique, a clinical laboratory test reagent, a polymerase chain reaction, a base sequence analysis and genetic engineering. The method enables the detection of a hepatitis-C virus having high carcinogenicity with high specificity. This sequence impresents the protein of the hepatitis-C virus NS3 gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hepatitis C virus peptide(s) and antibodies - used for immunoassays for hepatitis C virus or protective vaccines.
                                                                                                                                                                                                                                                                                                                                                                                     1 MSTNPKPORKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; HCV; epitope; core region; detection; vaccine.
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                                                                                                                                                                                                                                                                                    Length 3010;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                      100.0%; Score 501; DB 7; 100.0%; Pred. No. 3.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                91
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                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                RRQPI PKARR PEGRTWAQPGY PWPLYGNEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RROPIPKARRPEGRTWAQPGYPWPLYGNEGM
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                                                                                                                                                                                                                                                                                                                              91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus
                                                                                                                                                                                                                                                   Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-1993;
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02-MAR-1994
                                                                                                                                                                                                                 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR40978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
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                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                              datches
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                                                                                                                                                                                                                                                                                                                                                                                                          셤
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                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a partial Hepatitis C Virus (HCV) polyprotein from the non-structral region. Partial proteinase sequences (AAR82692-31) are contained within this sequence. The proteinases can be used as anti-HCV agents. They can also be used to screen cpds. for their ability to inhibit their proteolytic activity. In this way proteinase inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                        An HCV proteinase active substance - which has activity as an anti-HCV agent and can be used to screen for proteinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSTNPKPORKTKRNTNRRPODVKPPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing liver cancer, involves amplifying amino terminal region hepatitis-C virus gene using predetermined primer and determining hepatitis-C virus in base sequence of obtained DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      can be identified. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 501; DB 2; Length 3010;)
100.0%; Pred. No. 3.8e-45;
ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver cancer; hepatitis-C virus; NS3 gene; carcinogenicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus NS3 gene protein, SEQ ID No 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RROPIPKARRPEGRIWAOPGYPWPLYGNEGM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RRQPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 39-48; 52pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SHIN-) ZH SHINSANGYO SOZO KENKYU KIKO.
                                                                                                                                 (SUMQ ) SUMITOMO K.
(SUMQ ) SUMITOMO METAL IND LTD.
(SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
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                                                      92JP-00022657.
92JP-00249240.
92JP-00325303.
                    93JP-00018854.
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Best Local Similarity 100.
Matches 91; Conservative
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N-PSDB; ADF88596.
                                                                                                                                                                                                                 WPI; 1995-287962/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3010 AA;
                                                                                                                                                                                                                                     N-PSDB; AAT03960
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                                                        07-FEB-1992;
18-SEP-1992;
04-DEC-1992;
                      05-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-PEB-2004
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                                                                                                                9
                                                                                                                                                                 9
                                                                                                                                             1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic polypeptides from J1 and J7 hepatitis C virus isolates as immunoassay reagents, for raising antibodies and as vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV; non-A, non-B hepatitis; NANBH; diagnosis; vaccine; antigen; antibody; immunoassay; assay; core protein; envelope protein.
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     DB 2; Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Irvine BD, Kolberg JA, Han J,
                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C virus J7 isolate C/E consensus sequence.
  Score 498; DB 2;
Pred. No. 2e-46;
                                                                                                                                                                                                                          RROPIPKARRPEGRIWAOPGYPWPLYGNEGM 91
                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "Leu in clone 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Glu in clone 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "END in clone b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Thr in clone b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key Location/Qualifiers Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW30583 standard; protein; 154 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NAHE-) NAT INST OF HEALTH JAPAN
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89US-00456142.
91US-00637380.
93US-00101280.
94US-00201066.
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
  Query Match
Best Local Similarity 98.9
Matches 90; Conservative
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21-DEC-1989;
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nucleotide (see also AAX00400-04) sequences which are distinct from the HCV1 prototype. These differences can be exploited for use in diagnostics for NAMBH, recombinant protein production and vaccine development. Claimed HCV J1 and J2 polypeptide antigens can be used: (i) as immunoassay reagents, or standards, to detect HCV antibodies, e.g. for diagnosing infection or screening donated blood; (ii) to generate specific antibodies (used for detecting the corresponding polypeptide, to screen for antiviral agents, for virus isolation and for passive immunisation); (iii) in protective or therapeutic vaccines, and (iv) for isolation of non-A, non-B viruses
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98.9%; Pred. No. 3.3e-46;
Minnatches 0;
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-08-974-690C-187
US-07-681-701-16
US-08-143-579A-4
US-08-143-578A-4
US-08-454-928-8
US-08-454-195-2
US-08-65-883-2
US-09-127-829-2
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US-10-104-966-2
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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190,
180,
190,
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Patent No. 5882852...
GENERAL INFORMATION:

APPLICANT: BUKH, J., MILLER, R.H. AND.
APPLICANT: BUKH, J., MILLER, R.H. AND.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REACENTS DERIVED FROM THESE
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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Pred. No. 2.6e-51;
PCT-US95-10398-158
PCT-US95-10398-159
PCT-US95-10398-160
PCT-US95-10398-166
US-08-635-886C-179
US-08-635-886C-179
US-08-974-690C-179
US-08-977-597-50
US-08-977-597-50
US-08-927-597-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTONNEY, AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REPRENCE/DOCKET NUMBER: 2026-4116
TELECHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERRECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
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INDIVIDUAL ISOLATE: HK5
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STRANDEDNESS: unknown
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61 RRQPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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SOFTWARE: Patentin version 3.1
SEQ ID NO 187
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Best Local Similarity
Matches 91; Conserv
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Best Local Similarity
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US-08-635-886C-187
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                                           1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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NUCLEOTIDE AND DEDUCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPAITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
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    0; Indels
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100.0%; Pred. No. 2.6e-51;
tive 0; Mismatches 0;
                                                                                                                           61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
                                                                                                                                                  61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC CONMATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-ANG-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION NUMBER: 08/086,428
FILING DATE: 15-ANG-1993
PRIOR APPLICATION NUMBER: 08/086,428
FILING DATE: 15-ANG-1993
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          MILLER, R.H. AND
                                                                                                                                                                                                                                         T-US95-10398-173
Sequence 173, Application PC/TUS9510398
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 173:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acida
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE, DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (212) 758-4800
(212) 751-6849
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INDIVIDUAL ISOLATE: HKS
PCT-US95-10398-173
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Best Local Similarity 100.0
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                      APPLICANT: BUKH, J., MII
APPLICANT: PURCELL, R. H.
TITLE OF INVENTION: NUCL
TITLE OF INVENTION: COR!
TITLE OF INVENTION: COR!
TITLE OF INVENTION: SEQUENCES: 25CORRESPONDENCE ADDRESS:
      91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154
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      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: LEROUX-ROELS, Geert
APPLICANT: DELEXS, Robert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIRUS
TITLE OF INVENTION: VIRUS
FILE REPERENCE: 2551-94
CURRENT APPLICATION NUMBER: US/08/974,690C
CURRENT PILING DATE: 1997-11-19
PRIOR FILING DATE: 1997-11-19
PRIOR FILING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATENTING DATE: 1993-11-04
NUMBER OF SEQ ID NOS: 286
SOFTWARE: PATENTING DATE: 1993-11-04
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                                                                                                                              APPLICANT: DELEYS, ROBERT
APPLICANT: MAERTENS, Geert
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: IMMUNDOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
TITLE OF INVENTION: VIROS
TITLE REFERENCE: 2752-18
CURRENT PELING DATE: 1996-04-25
RIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: PCT/EP94/03555
PRIOR APPLICATION NUMBER: PCT/EP94/03556
PRIOR APPLICATION NUMBER: PCT/EP94/03556
PRIOR APPLICATION NUMBER: PCT/EP94/03556
PRIOR FILING DATE: 1993-110-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 501; DB 4; Best Local Similarity 100.0%; Pred. No. 7.3e-51; Matches 91; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
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Sequence 187, Application US/08635886C Patent No. 655114 GENERAL INFORMATION:
APPLICANT: LEROUX-ROELS, Geert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 187, Application US/08974690C
Patent No. 6613333
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6300 Columbia Center, 701 Fifth Avenue
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US-08-143-578A-4
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                                                            COUNTRY:
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TITLE OF INVENTION: CORE ANTIGEN PROTEIN OF HEPATITIS C
TITLE OF INVENTION: VIRUS, AND DIAGNOSTIC METHOD AND KIT USING THE SAME
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG 60
      1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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Pred. No. 5.8e-51;
1; Migmatches 0; Indels
                                                                                                                                                                            Sequence 16, Application US/07681701
Patent No. 5574132
- GENERAL INFORMATION:
APPLICANT: Lacroix, Martial
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17
CORRESPONDENCES: 17
CORRESPONDENCES: F15H & NEAVE
STREET: 875 THird Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FLIING DATE: 19910405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
                                                61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19910405
CLASSIFICATION: 530
ATTORNEY, AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: IAF-10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08143579A
Patent No. 5625034
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (212) 715-0742
(212) 715-0673
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TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 98.9
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-07-681-701-16
                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10022
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                US-07-681-701-16
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Sequence 4, Application US/08143578A
Sequence 1, Application US/08143578A
Sequence 1, Sequence 2, Sequence 3, TITLE OF INVENTION: CORE ANTIGEN PROTEIN OF HEPATITIS C
TITLE OF INVENTION: VIRUS, AND DIAGNOSTIC METHOD AND KIT USING THE SAME NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: Seed and Berry 5, STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 223;
                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,579A
PILING DATE: 26-0CT-1993
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION WHERE: US 07/963483
FILING DATE: 16-0CT-1992
ATTORNEY/AGENT INFORMATION:
NAME: King Joshus
REGISTRATION NUMBER: 35,570
REGISTRATION NUMBER: 35,570
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAK: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/143,578A
FILING DATE: 26-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 498; DB 1;
Pred. No. 7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.4%;
98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 3723836
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                     ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 223 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
COUNTRY: U.S.
ZIP: 98104-7092
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Gaps ..

Indels

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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                     1 MSTNPKPQRKTKRNTNRRPQDVKPPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MIYAMURA, TATSUO
APPLICANT: SAITO, IZUNO
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: HENATION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OSLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
CCUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: VIBJANASA

COUNTRY: U.S.A.

ZIP: 22202

ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Pacentin Release #1.0, Version #1.25
SOFTWARE: Pacentin Release #1.0, Version #1.25
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,195
FILING DATE: 05-UUN-1995
FILING DATE: 10-UUN-1995
APPLICATION NUMBER: US/08/446,303
FILING DATE: 11-UUN-1993
APPLICATION NUMBER: 22-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5799544man F.
RESISTRATION NUMBER: 24,618
FILING DATE: 11-UUN-1992
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (703) 413-2220
TELEFAX: (703) 413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SOIL IN SOIL INFORMATION:
TELEFAX: Z48855 OPAT UR
INFORMATION FOR SOIL INFORMATION:
SEQUENCE HARACTERISTICS:
TEMEX: TEMEX: 248855 OPAT UR
INFORMATION FOR SOIL INFORMATION:
TELEFAX: TANDAMATERISTICS:
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TEMEX: TANDAMER: TAND
                           98.9%; Pred. No. 7e-51;
tive 1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08462195; Patent No. 5789544
                           Best Local Similarity 98.9
Matches 90; Conservative
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Best Local Similarity
Matches 90; Conserv
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US-08-462-195-2
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APPLICANT: Liao, Jaw-Ching
APPLICANT: Liao, Jaw-Ching
TITLE OF INVENTION: DIAGNOSIS OF, AND VACCINATION AGAINST, A
TITLE OF INVENTION: POLYPEPTIDE ENCODED BY A SUBSTANTIALLY COMPLETE GENOME OF
TITLE OF INVENTION: SUCH VIRUS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY
STREET: 6300 Columbia Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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CITY: Seattle
STATE: Washington
CONTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPY disk
COMPUTER: 1BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,928
FILING DATE: 31-MAY-1995
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 310075.405
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-400
TELEPHONE: (206) 682-400
TELERAX: (206) 682-400
TELERAX: (206) 682-400
TELERAX: (205) 682-400
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                                                                                                                                         310075.402D2
ATTORNEY/AGENT INFO...

NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 31007
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEX: 3723836
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERSTICS:
LENGTH: CATA CATA
INFORMATION ACIDEN
TYPE: amino acide
TYPE: amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08454928
Patent No. 6153378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.91
Matches 90, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-143-578A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-454-928-8
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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
                                                                                                              1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG
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0
99.4%; Score 498; DB 1; Length 340; 98.9%; Pred. No. 1.2e-50; live 1; Mismatches 0; Indels
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Length 223;

DB 3;

99.4%; Score 498;

Query Match

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Sequence 2, Application US/09127829
Patent No. 6063904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400 CITY: Arlington STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                      APPLICANT: MITAMURA, TATSUO
APPLICANT: MATTAMURA, TATSUO
APPLICANT: SAITO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: HONDA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
TITLE OF INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INVENTION: HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/636,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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          61 RROPIPKARRPEGRTWAOPGYPWPLYGNEGM 91
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CLASSIFICATION NUMBER: US/US/080,083
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: US/US/446,303
PILING DATE: UJUN-1993
APPLICATION NUMBER: US 08/074,584
PILING DATE: 11-JUN-1993
APPLICATION NUMBER: JP 152487/1992
APPONEY FAGENT INFORMATION:
NAME: ODION, NO. 5830691man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 4169-003-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELEFRAX: (703) 413-2200
                                                          61 RROPIPKARRPEGRTWAOPGYPWPLYGNEGL
                                                                                                                                                                              Sequence 2, Application US/08636883
Patent No. 5830691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22202
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RESULT 11 US-09-127-829-2

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Patent No. 5882852
GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
APPLICANT: PURCELL, R.H.
ATTLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 498; DB 3; Length 340;
Pred. No. 1.2e-50;
                                                                                                                                                                                         NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
APPLICANT: MIYAMURA, TATSUO
APPLICANT: SAITO, IZUMU
APPLICANT: MATSUURA, YOSHIHARU
APPLICANT: MATSUURA, YOSHIKAZU
APPLICANT: SEKI, MAKOTO
TITLE OP INVENTION: METHOD FOR PRODUCING ECTOPROTEIN OF
TITLE OF INVENTION: HEPATITIS C VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                 STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: PLOSPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/446,303
FILING DATE:
APPLICATION NUMBER: US 08/074,584
FILING DATE: 11-JUM-1993
APPLICATION NUMBER: JP 152487/1992
FILING DATE: 11-JUM-1992
ATORNEY/AGENT INFORMATION:
NAME: Oblon, No. 6063904man F.
REGISTRATION NUMBER: 24,618
REGISCOMMUNICATION NUMBER: 4169-003-0
TELECOMMUNICATION INPORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.9%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (703) 413-3000
(703) 413-2220
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-09-127-829-2
                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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COUNTRY:
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Sequence INT, Application US/08290665A

Batent No. 5882852

GENERAL INFORMATION:
APPLICANT: BURGH, J., MILLER, R.H. AND
APPLICANT: BURCELL, R.H.
TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF THE ENVELOPE 1 AND
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HERATITIS C VIRUS
TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
NUMBER OF SEQUENCES: 263
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE TITLE OF INVENTION: SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES NUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
ADDRESSE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.2%; Score 497; DB 2; Length 191; 98.9%; Pred. No. 7.7e-51; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECHONE: (212) 758-4800
TELECHARE: (212) 751-6849
                                                                                                                                         STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: homosapiens
INDIVIDUAL ISOLATE: HK3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 98.9
nes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10154
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-290-665A-172
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Matches
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1 MSTNPKPORKTKRNTNRRPODVKPPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRG 60
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BUTCH, J., MILLER, R.H. AND
APPLICANT: PURCELL, R.H.
TITLE OF INVENTION: MUCLEOTIDE AND DEDUCED
TITLE OF INVENTION: CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: AND THE USE OF REAGENTS DERIVED FROM THESE
TITLE OF INVENTION: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%; Score 497; DB 2; Length 191; 98.9%; Pred. No. 7.7e-51; vative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RRQPIPKARQPEGRTWAQPGYPWPLYGNEGM 91
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,665A
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEX: 421792
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: unknown
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-AUG-1995
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290/665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
RPLING DATE:
FILING DATE:
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MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
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STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homosapiens INDIVIDUAL ISOLATE: HK4
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Best Local Similarity 98.9%
Marches 90; Conservative
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TITLE OF INVENTION: ANTH
TITLE OF INVENTION: CORE
TITLE OF INVENTION: SAUD
TITLE OF INVENTION: SEQUENCES: 263
CORRESPONDENCE ADDRESS:
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AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
AND THE USE OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.2%; Score 497; DB 5; Length 191; Best Local Similarity 98.9%; Pred. No. 7.7e-51; Matches 90; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BUKH, J., MILLER, R.H. AND
APPLICANT: BUKH, J., MILLER, R.H. AND
TITLE OF INVENTION: AUCLEOTIDE AND DEDUCI
TITLE OF INVENTION: AMINO ACID SEQUENCE;
TITLE OF INVENTION: CORE GENES OF ISOLATI
TITLE OF INVENTION: AND THE USE OF REAGER;
TITLE OF INVENTION: SEQUENCES IN DIAGNOST;
MUMBER OF SEQUENCES: 263
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10398
FILING DATE: 15-ANG-1995
CLASSIFICATION IN PROPER PRIOR APPLICATION NUMBER: 08/086,428
FILING DATE: 29 JUNE 1993
PRIOR APPLICATION NUMBER: 08/086,428
FILING DATE: 15 AUGUST 1994
ATTORNEY APPLICATION NUMBER: 08/086
FILING DATE: 15 AUGUST 1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459
REFERENCE/DOCKET NUMBER: 2026-4116
TELECOMMUNICATION INFORMATION:
                                                                                                            2026-4116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORGAN & PINNEGAN STREET: 345 PARK AVENUE CITY: NEW YORK STATE: NEW YORK COUNTRY: USA ZIP: 10154
FILING DATE: 15 AUGUST 1994

ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
REGISTRATION NUMBER: 36,459

REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELEX: 421792
INFORMATION FOR SEQ ID NO: 172:
SEQUENCE CHARACTERISTICS:
LENGTH: 191 amino acids
FYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
TOPOLOGY: unknown
ORIGINAL SOURCE:
ORGANISM: homosapiens
HONTUDUAL ISOLATE: HK3
PCT-US95-10398-172
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| TELEFAX: (212) 751-6849
| TELEFAX: 421792 | TELEFAX: 421792 |
| INFORMATION FOR SEQ ID NO: 174: |
| SEQUENCE CHARACTERISTICS: |
| LENGTH: 191 amino acids |
| TYPE: amino acid
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2005, 14:04:14; Search time 18:1106 Seconds (without alignments) 483.460 Million cell updates/sec

US-09-758-308-1 501 1 MSTNPKPQRKTKRNTNRRPQ......EGRTWAQPGYPWPLYGNEGM Perfect score: Sequence:

91

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	43	- CONTRACTOR OF THE CONTRACTOR	genome	denome	genome	genome		genome	hypothe	genome poly	structu	genome poly	genome		polypro	genome	genome polyp		polyprotein	депоше		162 genome polyprotein						
ΩH	24134	COMMISSION	512707	841341	841345	541346	JH0711	GNWVCH	S41342	841351	<b>JQ1584</b>	GNWVTC	S41344	S18031	PN0677	S18030	A44150	GNWVC3	841350	S41347	832740	\$214	PC1284	JQ1925	JQ1926	S19876	S41362	
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Query Match	0 00 0	0.00	0.00	0.66	99.0	99.0	99.0	99.0	98.6	98.2	98.2	98.2	97.8	97.6	97.6	97.6	97.4	97.4	97.2	97.2	97.2	97.2	96.8	96.8	96.8	96.8	96.4	
Score	100	100	1 0	496	496	496	496	496	494	492	492	492	490	489	489	489	488	488	487	487	487	487	485	485	485	485	483	
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genome polyprotein	polypeptide - hepa	genome polyprotein	genome polyprotein	genome polyprotein	genome polyprotein									
S41364 S41363	541368	S41349	S18032	A45573	S41365	S19875	S41370	S41348	GNWVTW	PC2219	S41357	JC5620	S41371	841369
01 0	10	7	~	ч	7	~	~	~	н	N	N	-	~	7
115	114	115	782	3010	114	782	114	108	3010	876	108	3014	112	114
95.6	95.4	95.2	95.0	95.0	94.8	94.8	94.6	94.4	94.4	94.2	94.0	93.8	93.0	95.6
479	478	477	476	476	475	475	474	473	473	472	471	470	466	464
30	35	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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S41343
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Substitute polyprotein - hepatitis C virus (genotype 1, N11) (fragment)
N;Contains: core protein
N;Contains: core protein
N;Contains: core protein
C;Species hepatitis C virus
A;Variety: genotype 1, N11
C;Date: 19-May-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004
C;Date: 19-May-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004
C;Date: 10-May-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004
C;Date: 10-May-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004
C;Date: 10-May-1994 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Molecule type: genomic RNA
A;Rossidues: 1-115 < VNAN>
A;Cross-references: UNIPROT: Q68877; EMBL: Z29446; NID: g443854; PIDN: CAA82584.1; PID: g443\*
C;Superimental source: genotype 1, NI1
C;Reywords: capaid protein; core protein; polyprotein
C;Reywords: capaid protein; matus predicted <AMT>

Gaps ö Length 115; Indels Query Match 100.0%; Score 501; DB 2; Best Local Similarity 100.0%; Pred. No. 8.8e-42; Matches 91; Conservative 0; Mismatches 0;

ö 9 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG ઠ

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61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGM 91 61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91 g ò

RESULT 2
GNWVCJ
GNWCJ
GNWC
GNWCJ
GNWC
GNWCJ
G

A; Modecule type: genomic RNA A; Residues: 1-3010 «KAT» A; Cross-references: UNIPPROT: P26662; GB: D90208; NID: g221610; PIDN: BAA14233.1; PID: g22161 R; Kato, N.; Obkoshi, S.; Shimocohno, K. Proc. Jpn. Acad. 658, 219-223, 1989

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Query Match
Best Local Similarity 100.0
Matches 90; Conservative
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Best Local Similarity 100.
Matches 90; Conservative
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N;Contains: core protein
C;Species: hepatitis C virus
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A; Residues: 1-115 < VAN>
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A; Reference number: PS0085
A; Reference number: PS0085
A; Reference number: PS0086
A; Molecule type senomic RNA
A; Residues: 2650-2707 «KA2>
C; Superfamily: hepatitis C virus genome polyprotein
F; 2-115/Product: envelope protein M #status predicted «MEE>
F; 192-389/Product: monstructural protein NS2 #status predicted «NS2>
F; 1007-1615/Product: nonstructural protein NS4 #status predicted «NS2>
F; 1312-1317/Region: nucleotide-binding motif B
F; 1316-1319/Region: DEXH motif
F; 1616-1319/Product: nonstructural protein NS5 #status predicted «NS5>
F; 1014-3010/Product: nonstructural protein NS5 #status predicted «NS5>
F; 1014-3010/Product nonstructural protein NS5 #status predicted «NS5>
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S12707
Genome polyprotein - hepatitis C virus (fragment)
N.Contains: core protein; envelope protein
C.Species: hepatitis C virus
C.Species: hepatitis C virus
C.Species: Jo.Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
Nucleic Acids Res. 18, 4626, 1990
A.Reference number: S12707, MUID: 90356432; PMID: 2117749
A.Reference number: S12707
A.Residues: 1-441 <- TAK>
A.Residues: 1-441 <- TAK>
A.Residues: 1-441 <- TAK>
A.Residues: 1-441 <- TAK>
Crosse-references: UNIPROT: Q81776; EMBL: D00574; NID: 9221656; PIDN: BAA00452.1; PID: 92216
C.Superfamily: hepatitis C virus genome polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome polyprotein - hepatitis C virus (genotype 1, N1) (fragment) N.Contains: core protein C;Species: hepatitis C virus A;Vařiety: genotype 1, N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 441;
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Pred. No. 6.2e-41;
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Best Local Similarity 98.9
Matches 90; Conservative
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Matches 91; Conserv
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C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: $41341
R;van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submirted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
A;Reference number: $41341
A;Roteusion: $41341
A;Roteule type: genomic RNA
A;Residues: 1-112 <VAN>A;Residues: UNIPROT:Q68875; EMBL:Z29444; NID:g443850; PIDN:CAA82582.1; PID:g4438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-115 <VAN>
A;Cross-references: UNIPROT:Q68879; EMBL:Z29448; NID:g443858; PIDN:CAA82586.1; PID:g4438
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C; Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C; Accession: S41346
R; van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A; Description: Analysis of hepatitis C virus genotypes 1 to 5 by LiPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Contains: core protein
C;Species: hepatitis C virus
A;Variety: genotype 1, N3
C;Date: 19-May-1994 #sequence_revision~26-Jul-1996 #text_change 09-Jul-2004
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K; van Doorn, L.G.; Kleter, G.E.M.; Brouwer, J.T.

submitted to the EMBL Data Library, January 1994

A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by

A;Reference number: $41341
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C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capsid protein; core protein; polyprotein
F;1-112/Product: core protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 2.6e-41; tive 0; Mismatches 0;
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C.Superfamily: hepatitis C virus genome polyprotein
C.Keywords: capsid protein; core protein; polyprotein
F1-115/Product: core protein #status predicted «MAT»
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100.0%; Pred. No. 2.7e-41;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 496; DB 2;
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A;Cross-references: UNIPROT: P27958; GB:M67463; NID:9329737; PIDN:AAA45534.1; PID:9329737; R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. R;Inchauspe, G.; Zebedee, S.; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. Proc. Natl. Acad. Sci. U.S.A. 88, 10292-10296, 1991

A;Title: Genomic structure of the human prototype strain H of hepatitis C virus: compary A;Reference number: A41546; MUID:92052256; PMID:1658800

A;Contents: annotation
A;Note: neither amino acid nor nucleotide sequence is given
C;Superfamily: hepatitis C virus genome polyprotein
C;Superfamily: hepatitis C virus genome protein
C;Superfamily: hepatitis C vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,2
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A; Experimental source: genotype 1, N10
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis core protein; polyprotein
P;1-115/Product: core protein #status predicted <MAT>
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C;Species: hepatitis C virus
A;Variety: genotype 1, N10
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
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submitted to the EMBL Data Library, January 1994
A;Description: Analysis of hepatitis C virus genotypes 1 to 5 by
A;Reference number: S41341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%; Score 496; DB 1; Length 3011; 100.0%; Pred. No. 6.1e-40; tive 0; Mismatches 0; Indels
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A,Molecule type: genomic RNA
A,Residues: 1-115 <VAN>
                                                                             A; Molecule type: genomic RNA A; Residues: 1-3011 <INC>
A; Reference number: A36814
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Matches 89; Conserv
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NiContains: envelope protein E1; envelope protein E2; nonstructural protein NS1; nonstructural protein NS1; nonstructural protein NS2; Species: hepatitis C virus

C;Species: hepatitis C virus

C;Species: hepatitis C virus

C;Date: 17-Apr-1993 #text_change 09-Jul-2004

C;Accession: JH0711

R;Liu, K.; Hu, Z.; Li, H.; Prince, A.M.; Inchauspe, G.

Gene 114, 245-250, 1992

A;Tile: Genomic typing of hepatitis C viruses present in China.

A;Reference number: JH0711; MUID:92290283; PMID:1318245

A;Reference number: JH0711; MUID:92290283; PMID:1318245

A;Residues: 1-550 <LIU>
A;Rolecule type: genomic RNA

A;Residues: 1-550 <LIU>
A;Rolecule type: genomic RNA

A;Residues: 1-550 <LIU>
A;Rolecule type: genomic RNA

A;Residues: 1-550 <LIUS

A;Note: the nucleotide sequence is not complete

C;Superfamily: hepatitis C virus genome polyprocein

C;Superfamily: hepatitis C virus genome polyprocein

C;Keywords: envelope protein; glycoprotein; nonstructural protein; nonstructural protein R; #status Felils-190/Product: envelope protein E2 or nonstructural protein NS1 (fragment) #status P; F;381-514/Product: envelope protein E2 or nonstructural #status predicted <ANS5>

F;196, 233, 250, 305, 416, 422, 429, 447/Binding site: carbohydrate (Asn) (covalent) #status pr
        A;Reference number: S41341
A;Accession: S41346
A;Accession: S41346
A;Accession: S41346
A;Allele type: genomic RNA
A;Residues: 1-118 <VAN>
A;Cross-references: UNIPROT:Q68880; EMBL:Z29449; NID:g443860; PIDN:CAA82587.1; PID:g4438
A;Experimental source: genotype 1, N4
C;Superfamily: hepatitis C virus genoe polyprotein
C;Keywords: capaid protein; core protein; polyprotein
F;1-118/Product: core protein #status predicted <AMT>
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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A; Note: host Home sapiens (man)
C; Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C; Accession: A36814; A41546
R; Inchauspe, G; Zebedee, S; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Pred. No. 1.2e-40;
                                                                                                                                                                                                                                                                                                                                                                                                    Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                    'Match 99.0%; Score 496; DB Local Similarity 100.0%; Pred. No. 2.7 tes 90; Conservative 0; Mismatches
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90; Conservative
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Matches 90; Conserv
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Matches 90
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; DB 2; Length 115; 4.2e-41; 1; Indels

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A; Molecule type: genomic RNA
A; Residues: 1-3010 cTAK>
A; Residues: 1-3010 cTAK>
A; Residues: 1-3010 cTAK>
Cross-references: UNIPROT: P26663; EMBL: M58335; NID: 9329770; PIDN: AAA72945.1; PID: 93297
C; Superfamily: hepatitis C virus genome polyprotein
C; Reywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura
C; Reywords: ATP; capsid protein C #status predicted <PEP>
F; 12-115, Product: envelope protein M #status predicted <BPM>
F; 192-389, Product: molor envelope protein B #status predicted <MEE>
F; 390-729, Product: nonstructural protein NS1 #status predicted <NS1>
F; 1007-1615, Product: hepacivirin #status predicted <NS2>
F; 1230-1237, Region: nucleotide-binding motif B
F; 1312-1317, Region: nucleotide-binding motif B
F; 1312-1317, Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;18014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196, 209, 234, 250, 305, 325, 417, 423, 430, 446, 532, 540, 556, 576, 623, 645, 1213, 1255, 2041, 2077, 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome polyprotein - hepatitis C virus (genotype 1, N2) (fragment)
N;Contains: core protein
C;Species hepatitis C virus
N;Contains: core protein
C;Species hepatitis C virus
A;Variety: genotype 1, N2
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Date: 10-May-1994 #sequency
A;Reference number: S41344
A;Reference number: S41341
A;Reference number: S41344
A;Molecule type: genomic RNA
A;Residues: 1-115 < vAN>
A;Cossidues: 1-115 < vAN>
A;Coss-references: UNIPROT: Q68878; EMBL: Z29447; NID: g443856; PIDN: CAA82585.1; PID: g4438
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: capaid protein; core protein; polyprotein
F;1-115/Product: core protein #status predicted <MAT>
(nonstructu
                                                                                                                                                                 R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe, S.; Murakami, S.; Fujita, J.; Onishi, E.; J. Virol. 65, 1105-1113, 1991
A;Title: Structure and organization of the hepatitis C virus genome isolated from human A;Reference number: A38465; MUID:91140698; PMID:1847440
A;Accession: A38465
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                                   protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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                                                                          C;Species: hepatitis C virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
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Pred. No. 1.5e-39;
1; Mismatches 1.
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; Pred. No. 1e-40
0; Mismatches
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97.8%;
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Matches 89; Conservative
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                         C; Accession: A38465
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JQ1584
genome polyprotein - hepatitis C virus (strain U.K.) (fragment)
N;Contains: core protein C; envelope protein E1; envelope protein E2; nonstructural prot
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: J7-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JQ1584
C;Accession: JQ1584
D; Thomas, H; Monjardino, J.
J; Gen. Virol. 73, 1521-1525, 1992
A;Title: Cloning and sequencing of the structural region and expression of putative core
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Reference number: JQ1584; MUID:92300349; PMID:1318944
A;Residues: 1-640 «KUM»
A;Residues: 1-640 «KUM»
A;Residues: 1-640 «KUM»
A;Residues: UNIPROT:Q68966; GB:X84079; NID:g643119; PIDN:CAA58888.1; PID:g643126
C;Superfamily: hepatitis C virus genome polyprotein; nonstructural protein; polyprocie; c;Keywords: core protein; envelope protein; glycoprotein; nonstructural protein; polyprocie; F;191/Product: envelope protein E2 and nonstructural protein NSI #status predicted «EE1»
F;390-640/Product: envelope protein E2 and nonstructural protein NSI #status predicted *F;196,209,234,305,417,430,448,476,540,556,576,623/Binding site: carbohydrate (Asn) (cova
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                                                                                                          genome polyprotein - hepatitis C virus (genotype 1, N9) (fragmen C) Species: hepatitis C virus
N; Contains: core protein
C; Species: hepatitis C virus
A; Variety: genotype 1, N9
C; Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change
C; Accession: 841351
R; van Doorn, L.J.; Kleter, G.E.M.; Brouwer, J.T.
submitted to the EMBL Data Library, January 1994
A; Description: Analysis of hepatitis C virus genotypes 1 to 5 by
A; Reference number: 841341
A; Residues: 1-115 < VAN>
A; Residues: 1-115 < VAN>
A; Coss-references: UNIPROT: Q68885; EMBL: Z29454
A; Cross-references: UNIPROT: Q68885; EMBL: Z29454
C; Superimental source: genotype 1, N9
C; Superimental source: genotype
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Pred. No. 6.5e-41;
1; Mismatches 1;
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Best Local Similarity 97.8%;
Matches 89; Conservative
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RROPIPKARRPEGRIWAQPGYPWPLYGNEG 90

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S18031
Strong polyprotein - hepatitis C virus (isolate JK2) (fragment)
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
N;Contains: core protein; envelope protein 1; nonstructural protein 2; NS1/E2 protein
A;Variety: isolate JK2
C;Species: Appailits C virus
A;Variety: isolate JK2
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: S18031
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
R;Honda, M.; Kaneko, S.; Masashi, U.; Kobayashi, K.; Murakami, S.
A;Reference number: S18029
A;Reference number: S18029
A;Recession: S18031
A;Molecule type: genomic RNA
A;Residues: 1-782 -HON>
A;Cross-references: UNIPROT: Q68950; EMBL: X61593
A;Experimental source: isolate JK2
C;Superimental source: isolate JK3
F;1-191/Product: core protein #status predicted <AMT2>
F;1-191/Product: NS1/E2 protein #status predicted <AMT2>
F;134-733/Product: nonstructural protein 2 (fragment) #status predicted <AMT4>
F;734-782/Product: nonstructural protein 2 (fragment) #status predicted
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Accession: PN0677
R;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
B;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
B;Cho, S.H.; Yoon, J.I.; Chang, J.E.; Ahn, B.M.; Lee, C.H.; Lee, Y.I.
A;Chomic typing of hepatitis C viruses from patients: Implications of gen
A;Reference number: PN0677; MUID: 94059104; PMID: 8240354
A;Accession: PN0677
A;Molecule type: mRNA
A;Residues: 1-787 <CHO>
A;Chos-references: UNIPROT: Q08244; GB: L20498; NID: g1381031; PIDN: AAB02608.1; PID: g13810
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: g1ycoprotein; nonstructural protein
F;196,209,234,250,305,325,421,427,452,536,544,560,580,627,649/Binding site: carbohydrate
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A natural intergenotypic recombinant of hepatitis C virus identified in St. Petersburg.", To set 1 to 
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Core protein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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                                                                                                                                               Last sequence update)
Last annotation update)
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100.0%; Pred. No. 3.1e-43;
tive 0; Mismatches 0;
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100 AA
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MEDLINE=21904745; PubMed=11907242;
DOI=10.1128/JVI.76.8.4034-4043.2002;
Kalinina O., Norder H., Mukomlov S.,
                                                                                                  Created)
                                                                                         01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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    PRELIMINARY;
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Hepatitis C virus.
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Hepacivirus
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                                                                                                             MEDLINE=21904745; PubMed=11907242;
DOI=10.1128/JVI.76.8.4034-4043.2002;
Kalinina O., Norder H., Mukomolov S., Magnius L.O.;
"A natural intergenotypic recombinant of hepatitis C virus identified
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Kallnina O., Norder H., Mukomolov S., Magnius L.O.;
"A natural intergentypic recombinant of hepatitis C virus identified
in St. Petersburg-";
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Pred. No. 3.1e-43;
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J. Virol. 76:4034-4043(2002).
EMBL, AY070205; AALS8619.1;
PIR; PQ0804; PQ0804.
HSSP, Q8JYS1; ICWX.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; P:structural molecule activity; IEA.
InterPro; IPR002522; HCV capsid.
Pfam; PP01543; HCV capsid.
NON TER.
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EMBL, AX070200, AAL58614.1; -.
HSSP, QGUYSI, 1CWX.
GO, GO:0019028, C:viral capsid; IEA.
GO, GO:0005198; F:structural molecule activity; IEA
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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MEDLINE=21904745; PubMed=11907242;
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Pfam; PF01543; HCV capsid; 1.
NON TER 100
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Hepatitis C virus.
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                                                                     SEQUENCE FROM N.A
                        NCBI_TaxID=11103;
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NCBI_TaxID=11103;
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01-JUN-2002
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01-OCT-2003
Hebacivirus
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1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQ1VGGVYLLPRRGPRGVRLGVRATRKTSERSQPRG
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EMBL: Z29446; CAA82584.1; -.

PIR: PQ0804; PQ0804.

PIR: S41343; S41343.

HSSP: Q8JYSI: 1CWX.
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Hepatitis C virus type 1.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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PubMed=14718617; DOI=10.1099/vir.0.19472-0;
Colina R., Casane D., Vasquez S., Garcia L., Chunga A., Romero H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97201609; PubMed=9049395; Maertens G., van Doorn L.J., Kleter B.G.E.M., Stuyver L., Maertens G., van Doorn L.J., Kleter B.G.E.M., Heijtink R.A., Quint W.G.V.; Brouwer J.T., Schalm S.W., Heijtink R.A., Quint W.G.V.; "Sequence analysis of Hepatitis C virus genotypes 1 to 5 reveals multiple novel subtypes in the Benelux countries.";
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR00522: HCV capsid.
Pfam; PF01543; HCV capsid; 1.
NON TER 115 115
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Last annotation update)
                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                 (genotype 1, B75) core region RNA (Fragment). Hepatitis C virus.
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61 RROPIPKARRPEGRIWAQPGYPWPLYGNEGM 91
                           61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
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MEDLINE=96048319; PubMed=8551256;
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91; Conservative 0
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Best Local Similarity
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Local Similarity 100.
nes 91, Conservative
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                                   PRELIMINARY;
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CHAIN
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Q8JWN3
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MEDLINE=22241990; PubMed=12354856;
Ogata S., Nagano-Pujii M., Ku Y., Yoon S., Hotta H.; Its frameshift "Comparative sequence analysis of the core protein and its frameshift product, the F protein, of hepatitis C virus subtype 1b strains obtained from patients with and without hepatocellular carcinoma."; J. Clin. Microbiol. 40:3625-3630(2002).
EMBL; PO0804; PO0804.
HSSP; Q8JXS1; 1CWX.
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Hepacivirus; Hepatitis C virus type 1.
NCBI_TaxID=31647;
Kahn B., Cristina J.;
"Genetic analysis of Hepatitis C viruses in Peruvian patients.";
"Gonetic analysis of Hepatitis C viruses in Peruvian patients.";
"Go. Go. Virol. 85:31-37(2004).
EMBL; AJ582130; CRE46586.1;
"GO; GO:0019028; CRE46586.1;
"GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR013531; HCV_capsid.
Pfam; PF01543; HCV_core; I.
Pfam; PF01542; HCV_core; I.
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GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
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Last annotation update)
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Pred. No. 6.2e-43;
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100.0%; Pred. No. 4.3e-43;
ive 0; Mismatches 0;
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Pfam; PF01542; HCV core; 1.
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Hepatitis C virus type 1b.
                                                                                                                                   Local Similarity 100.
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SEQUENCE
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Matches
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MEDLINE=22241990; PubMed=12354856;

MEDLINE=22241990; PubMed=12354856;

MEDLINE=22241990; PubMed=12354856;

MEDLINE=22241990; PubMed=12354856;

"Comparative sequence analysis of the core protein and its frameshift product, the F protein, of hepatitis C virus subtype 1b strains obtained from patients with and without hepatocellular carcinoma."; J. Cilu. Microbiol. 40:3625-3630(2002).

EMBL; AB077712; BAC02447.1; -. EMBL; AB077712; BQ084; PQ0804.

HSSP; Q8945; PQ0804.
                                                                                                                                                                                                                                                                                                                      MEDLINE=2241990; PubMed=12354856; Ogata S., Notta H.; Ogata S., Nagano-Fujii M., Ku Y., Yoon S., Hotta H.; Ogata S., Nagano-Fujii M., Ku Y., Yoon S., Hotta H.; Comparative sequence analysis of the core protein and its frameshift product, the F protein, of hepatitis C virus subtype 1b strains obtained from patients with and without hepatocellular carcinoma."; J. Clin Microbiol. 40:3625-3630(2002).

EMBL; AB077715; BAC02450.1; -.
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Hepatitis C virus type 1b.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                        01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus type lb.
Viruses; SSRNA positive-skrand viruses, no DNA stage; Flaviviridae;
Hepativus; Hepatitis C virus type 1.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
InterPro; IPR002521; HCV_capsid.
InterPro; IPR002521; HCV_core.
Pfam; PF01543; HCV_core; 1.
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191 AA
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PRT;
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1 MSTNDKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRG 60
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                            Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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Viruses; ssRNA positive-strand viruses, no DNA stage, Flaviviridae,
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062232; BAB83426.1; -.
PIR; PQ0804; PQ0804.
HSSP; Q8JYS1; LCWX.
GO; GO:019028; C:structlarl molecule activity; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
NON TER
SEQÜENCE 191 AA; 20774 MW; 9D33D9B93B848A31 CRC64;
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PIR; PQ0804; PQ0804.
HSSP; Q8JYE1; 1CWX.
GO; GO:0013028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
PEam; PF01543; HCV_core; 1.
NON TER 191 191
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100.0%; Pred. No. 6.2e-43;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 91; Conservative
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nes 91; Conservative
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TISSUE=Liver;
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TISSUE-Blood;
Kato N.;
Ka
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191 AA; 20796 MW; 93DD39B92A7E8031 CRC64;
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GO:0005198; F:structural molecule activity; IEA.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
Core protein (Fragment).
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                                                                                                                                                                                                                                             core protein.
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                                InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01542; HCV_core; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      91; Conservative
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NCBI_TaxID=11103;
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01-MAR-2002 (
01-MAR-2002 (
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Q8V7P2;
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kato N.;
Submitted (Mar. 2001) to the EMBL/GenBank/DDBJ databases.
Submitted (Mar. 2001) to the EMBL/GenBank/DDBJ databases.
EMBL, ABG6228; BAB83422.1; -.
PIR, PQ0804; PQ0804.
R GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
R GO; GO:0005198; F:structural molecule activity; IEA.
R Pfam; PPO1543; HCV capsid; 1.
R Pfam; PFO1542; HCV core; 1.
I NON IER 191
T SEQÜENCE 191 AA; 20808 MW; 93DD39B93B8E8031 CRC64;
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EMBL, AB062227; BAB83421.1; -.
PIR, PQ0804; PQ0804.
HSSP; Q87YE; 1.CWX.
GO; GO:0019028; C:viral capsid; IEA.
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100.0%; Pred. No. 6.2e-43;
tive 0; Mismatches 0;
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Best Local Similarity
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NCBI_TaxID=11103;
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Kato N.;
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
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Hepacivirus.
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100.0%; Score 501; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.2e-43;
Matches 91; Conservative 0; Mismatches 0; Indels
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB062229; BAB83423.1; -.
PIR; PQ0804; PQ0804.
HSSP; QBJYS1; 1CWX.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:001928; F:structural molecule activity; IEA.
Pfam; PP01543; HCV capsid; 1.
Pfam; PP01542; HCV core; 1.
Pfam; PP01542; HCV core; 1.
NOW TER 191 AA; 20808 MW; 93DD39B93B8EB031 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0005198; E:structural molecule activity; IEA.
Pfam; PF01543; HCV capsid; 1.
Pfam; PF01542; HCV core; 1.
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Best Local Similarity 100.0%; Pred. No. 6.2e-43;
Matches 91; Conservative 0; Mismatches 0;
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PIR; PQ0804; PQ0804.
HSSP; Q8JYS1; ICWX.
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                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25,
                                   PRELIMINARY;
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TISSUE=Liver;
                                                                                                                                                                           Hepatitis C virus.
                                                                                                                                                                                                                                   NCBI_TaxID=11103;
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Kato N.;
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RESULT 12
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Query Match
100.0%; Score 501; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.2e-43;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps
GO; GO:0005198; F:structural molecule activity; IEA. Pfam; PF01543; HCV_capsid; 1. PFam; PF01542; HCV_core; 1. NON TER 191 191 SEQÜENCE 191 AA; 20808 MW; 93DD39B93BBEB031 CRC64;
                                                                                                                                                                                                            61 RRQPIPKARRPEGRTWAQPGYPWPLYGNEGM 91
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The present sequence represents an antigenic epitope from a hepatitis C virus (HCV) NS4 protein. The peptide comprises amino acids 1789-1867 of the HCV polyprotein. The specification describes antigenic epitopes from HCV core protein, NS3 protein, NS4 protein and NS4a protein. The antigenic peptides are useful as diagnostic reagents for detecting HCV in a biological sample. They are also useful for monitoring HCV infection in a patient sample in addition to diagnosis. Pharmaceutical compositions comprising the peptides are useful for preventing, minimizing or reducing HCV infection in patients who have been exposed to HCV or to individuals, such as health care workers or blood product recipients, who are more likely to become exposed to HCV infection. The antigenic peptides are also useful for generating antibodies which can be used to detect HCV proteins in a sample or for laboratory research purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New (mosaic) polypeptides, useful as reagents in assays for the diagnosis or monitoring of HCV infections and as components of anti-HCV vaccines, comprises antigenic groups of hepatitis C virus (HCV).
                                                            Recombina
Non-A, no
Non-A, no
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HCV-S1 fu
OSPF-rela
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Hepatitie
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                    Aay70064
Aay70065
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Aar20011
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Abu09574
Abu09575
Adr38450
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Aar29907
Aar58591
Adl17782
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AAW01680
AAY70064
AAY70066
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AAX200911
AAY6423
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  WO200104149-A1.
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  AAB31697;
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  HCV polyp
Hepatitis
HCV NS2-N
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HCV NS2-N
HCV NS2-N
HCV NS2-N
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PT-NANBH
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HCV NS2-N
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368.645 Million cell updates/sec
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                                                                                                                                                    August 12, 2005, 14:00:18 ; Search time 82.8821 Seconds
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Aar68622 B
Aar29533 B
Aar34580 B
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Aar29846 F
Aab36932 F
                                                                                                                                                                                                                                                                                   1 SVVIVGRIILSGRPAVIPDR......TATKQABAAAPVVBSKWRAL
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Aaw412863
Aaw412863
Aar29866
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Aar29660
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                               2105692 segs, 386760381 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              - protein search, using sw model
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AAR29866
AAR29867
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Maximum DB seg length: 2000000000
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Result No.

Post-processing:

Database

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

us-09-758-308-3.rag

Best Loc Matches

8 ò

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RESULT 2

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Hepatitis C virus antigen expressed as recombinant in E.coli - useful for diagnosis of hepatitis C virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in AAR25854-74 are hepatitis C virus protiens. The genes encoding these proteins can each be used to prepare recombinant vectors by ligating the gene of interest in to a vector to be expressed in E. coli. These polypeptides are useful as diagnostic reagents for type C hepatitis and they may be produced efficiently by recombinant methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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                                                                        Recombinant vector; E. coli; diagnostic; reagent; type C hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 394; DB 2; Length 195; 100.0%; Pred. No. 1.5e-41; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW41741 standard; protein; 195 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 3-4; 66pp; Japanese.
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            21-JAN-1993 (first entry)
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Best Local Similarity 100...
Best Aca 79; Conservative
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(GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                             (TOKU ) TOKUYAMA SODA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis; detection
                                                                                                                                                                                                                                                                                            WPI; 1992-263663/32.
                                           HCV polypeptide 10.
                                                                                                       Hepatitis C virus
                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ26990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 195 AA;
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                                                                                                                                      JP04179482-A
                                                                                                                                                                     26-JUN-1992.
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                                                                                                         1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus; HCV; antigen; diagnosis; reagent; agglutination.
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                                          100.0%; Score 394; DB 4;
100.0%; Pred. No. 4.4e-42;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2-3; Page 17-18; 18pp; Japanese.
                                                                                                                                                                                                                                                                              AARS2737 standard; protein; 194 AA.
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                                                          Local Similarity 100.
1es 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 194 AA;
            Sequence 79 AA;
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                                                                                                                                                                                                                                                                                                                                                                          HCV antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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AAR25863

RESULT 3

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Gaps

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The sequences given in AAR29852-70 are encodeed by various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention (see also AAR2660, AAR295559-60 and AAR29843-51). These RNA sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                        - used for diagnosing
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                                                                                 1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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Length 293;
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                                        Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hepatitis C virus gene and its encoded protein and vaccinating against hepatitis C virus infections
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100.0%; Pred. No. 4.8e-41;
tive 0; Mismatches 0;
100.0%; Score 394; DB 2;
100.0%; Pred. No. 2.5e-41;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 172-75; 305pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcriptase; cDNA; primer; allele.
                                                                                                                                                                                                                                                                                                               AAR29866 standard; protein; 477 AA.
                                                                                                                                                                                                      ATKOAEAAPVVESKWRAL 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV NS2-NS4 peptide N16N15B-1.
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                                                                                                                                                                  ATKQAEAAAPVVESKWRAL
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91JP-00332329
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(first entry)
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Best Local Similarity 100.0
Matches 79; Conservative
                     Best Local Similarity 100.
Matches 79; Conservative
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07-OCT-1991;
16-DEC-1991;
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26-APR-1993
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      Query Match
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                                                                                                                                                                                                                                                                                            AAR29866
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                                                         Protein contg. non-B hon-B hepatitis antigen fragment - prepd. by culturing transformants transformed by vector contg. base sequence coding specified aminoacid sequences, used for detecting hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                     76 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequences given in AAR98349-50 represent antigenic peptides which were derived from the NS3 and NS4 proteins of hepatitis C virus (HCV), respectively. These peptides were used in the preparation of novel antibodies. The antibodies were prepared by immunising a bird with one of the peptides and isolating the resulting antibody from the egg yolk of eggs laid by the immunised bird. The antibodies may be used in the detection of HCV antigens in the blood and are useful in the development of diagnostic agents or drugs for hepatitis C. The antibody is highly specific and as the peptide is injected without a carrier protein, only anti-NS3 or anti-NS4 antibodies are produced
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                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                     The present sequence is a non-A non-B hepatitis virus (NANBH) or hepatitis C virus (HCV) antigen, useful for diagnosis or detection
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                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 394; DB 2; Length 195;
Best Local Similarity 100.0%; Pred. No. 1.5e-41;
Matches 79; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATKQAEAAPVVESKWRAL 79
                                                                                                                                                 Claim 1; Fig 7; 53pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94JP-00264808
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                         WPI; 1993-260858/33.
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297 ATKQAEAAAPVVESKWRAL 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 296
1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFXQXALGLLQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
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                                                                                                                                                      AAR29867 standard; protein; 477 AA
                                                               297 ATKQAEAAAPVVESKWRAL 315
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                                             ATKQAEAAPVVESKWRAL 79
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1es 79; Conservative
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12-JUL-1991;
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The sequences given in AAR29852-70 are encodeed by various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C virus (HCV) gene of the invention (see also AAR29560, AAR29559-60 and AAR29843-11. Theses RNA sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)

    used for diagnosing

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iive 0; Mismatches 0;
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AAR29865 standard; protein; 477 AA.
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                                                                                                                                                                         HCV NS2-NS4 peptide N16N15A-1.
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Matches 79; Conservative
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The sequences given in AAR29660, AAR29559-60 and AAR29843-51 were encoded by clones which encode the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The NS2-NS4 RNA sequences were converted into cDNA using transcriptes in the presence of one of the primer sequences given in AAQ32553-64. The cDNA sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAQ3236. (Updated
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                                                            Clone; polypeptide; NS2-NS4; Hepatitis C; Virus; HCV; serum; HC; transcriptase; cDNA; primer; allele.
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26-APR-1993 (first entry)
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N-PSDB; AAQ32481.
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16-DEC-1991;
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 The sequences given in AAR29852-70 are encodeed by various clones which were used in the isolation of the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention (see also AAR29660, AAR29559-60 and AAR29843-51). These RNA sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into coNA using transcriptase in the presence of one of the primer sequences given in AAQ32578-79. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAQ32436. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murakami T, Teranishi Y, Hayashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 SVVIVGRIIISGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                  Clone, polypeptide, NS2-NS4; Hepatitis C, Virus; HCV; serum; HC;
transcriptase, cDNA; primer; allele.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 394; DB 2;
Pred. No. 9.1e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Page 178-82; 305pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; protein; 768 AA
   AAR29868 standard; protein; 768 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                 HCV NS2-NS4 peptide N23N15A-1.
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91JP-00287008.
91JP-00332329.
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                                                                   (revised)
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Best Local Similarity
The 79; Conservê
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1992-417213/51.
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                                                                                                                                                                                                  Hepatitis C virus
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12-JUL-1991;
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16-DEC-1991;
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                                                                   25-MAR-2003
26-APR-1993
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Hayashi N;

Teranishi Y,

(revised)

25-MAR-2003

AAR29850;

AAR29850

RESULT 10 AAR29850

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Gaps

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Indels

587 9

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RESULT 11 **AAR**29869

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1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
                                                                                                                                                                                                                                                                                                                            Clone, polypeptide, NS2-NS4, Hepatitis C; Virus, HCV, serum, HC, transcriptase, cDNA, primer, allele.
Best Local Similarity 100.0%; Pred. No. 9.1e-41; Matches 79; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Asn, Arg, Lys
                                                                                                                                                                                                   AAR29660 standard; protein; 1188 AA
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Len
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Gly, Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Leu, Ile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Leu, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Ala, Val
                                                                                                                  79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= Thr,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Met,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Asp,
                                                                                                  61 ATKOAEAAAPUVESKWRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Ala,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Phe,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Asp,
                                                                                                                                                                                                                                                                                                     HCV NS2-NS4 peptide MX25N15.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 267
                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
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                                                                                                                                                                                                                                                           25-MAR-2003
26-APR-1993
                                                                                                                                                                                                                                 AAR29660;
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                                                                                                                                   1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                         Clone, polypeptide, NS2-NS4, Hepatitis C, Virus, HCV; serum, HC, transcriptase, cDNA, primer, allele.
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                                                           Length 768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Teranishi Y,
                                                                                      Indels
                                                        100.0%; Score 394; DB 2;
100.0%; Pred. No. 9.1e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murakami T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 182-86; 305pp; English.
  on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                            AAR29869 standard; protein; 768 AA
                                                                                                                                                                                             588 ATKOAEAAAPVVESKWRAL 606
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91JP-00287008.
91JP-00332329.
                                                                                                                                                                                                                                                                                                                                                                             HCV NS2-NS4 peptide N23N15B-1
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                                                                                                                                                                         ATKQAEAAAPVVESKWRAL
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(first entry)
                                                                         Best Local Similarity 100.
Matches 79; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus
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                               Sequence 768 AA;
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07-OCT-1991;
16-DEC-1991;
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26-APR-1993
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                                                           Query Match
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100.0%; Score 394; DB 2; Length 768;

Query Match

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Gaps

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Indels

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Conservative

Query Match Best Local Similarity T9; Conserv?

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Sequence 1188 AA;

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100.0%; 100.0%;

Score 394; DB 2; Pred. No. 1.6e-40; Mismatches 0;

Length 1188;

9

948 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 1007

ATKQAEAAAPVVESKWRAL 79

61

1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT

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New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                            Murakami T, Teranishi Y, Hayashi N;
                                                                                                                                                                           label= Val, Ile
                                                                                                                                                                                                                                       'label= Thr, Ala
       label= Ile, Leu
                     label= Leu, Phe
                                                                  label= Leu, Pro
                                                                                 label= His, Arg
                                                                                                              label= Ser, Thr
                                                                                                                                                                                                                       label= Glu, Lys
                                                                                                                                                                                                                                                      /label= Tyr, Phe
                                                                                                                                                                                                                                                                     /label= Thr, Ala
                                                                                                                                                                                                                                                                                                                                                                                            Seki M, Honda Y, Takahashi K,
                                                                                                                                                                                                                                                                                                                                       91JP-00172794.
91JP-00287008.
91JP-00332329.
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                                                                                                                             label= Lys,
                                     label= Ile,
                                                   label= Gly,
                                                                                                abel= Thr,
                                                                                                                                             label= Ile,
                                                                                                                                                            label= Thr,
                                                                                                                                                                                          label= Pro,
                                                                                                                                                                                                         label= Tyr,
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N-PSDB; AAQ32442.
                             Misc-difference 343
               Misc-difference 281
Misc-difference
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07-OCT-1991;
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This sequence was encoded by the Hepatitis C Virus (HCV) gene of the invention. The HCV gene is useful in the development of a diagnostic method which is more accurate and effective than conventional ones, in the detection of antibodies raised against a wide range of HCVs which have been hardly detected before. The complete gene may be used in an invitro screening system for a substance capable of specifically supressing or controlling a proteolytic processing of a precursor polypeptide of HCV. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi N;
                                                                                                                                                                                               Clone; Hepatitis C Virus; HCV; core-envelope; NS1(gp70); NS2-NS4; NS4-NS5; region; diagnostic method; antibody; supress; control; process; precursor; polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Teranishi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hepatitis C virus gene and its encoded protein - and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murakami T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1 and 3; Page 259-272; 305pp; English
                                                                                                                                                                                                                                                                                                           /note= "Nonsense codon"
                                                                           AAR29527 standard; protein; 2510 AA
                                                                                                                                                                                                                                                                                 Location/Qualifiers
1008 ATKQAEAAAPVVESKWRAL 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takahashi K,
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                                                                                                                                                                                                                                                                                                Misc-difference 2212
                                                                                                                                                                         HCV antigen T7N1-30
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                                                                                                                                                                                                                                                       Hepatitis C virus
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07-OCT-1991;
16-DEC-1991;
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                                                                                                       AAR29527;
                                                   RESULT 13
                                                                AAR2952
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Length 2510;

Score 394; DB 2; Pred. No. 4.4e-40;

100.0%; 100.0%;

Query Match Best Local Similarity

The sequences given in AAR29660, AAR29559-60 and AAR29843-51 were encoded by clones which encode the NS2-NS4 regions of the Hepatitis C Virus (HCV) gene of the invention. These sequences were isolated from the serum of a patient suffering from hepatitis C (HC). The NS2-NS4 RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32553-64. The cDNA sequences were then amplified using primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence comparisons of these clones showed that it is possible for a patient to carry more than one HCV strain at one time. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)

Disclosure; Page 139-45; 305pp; English

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JP07184648-A.
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       18-SEP-1992;
                    18-SEP-1992;
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04-DEC-1992;
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14-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                               Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                            RESULT 15
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                       1679 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 1738
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              1 SVVIVGRIILSGRPAVIPDREVLYQEPDEMBECASHLPYIEQGMQLAEQFKQKALGLLQT
 Gaps
                                                                                                                                                       Hepatitis C virus; HCV; non-A non-B; helicase gene; RNA helicase; baculovirus; recombinant production.
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0; Indels
                                                                                                                                                                                                                  209. .211
//abela N-linked glycosylation site
234. .236
//abela N-linked glycosylation site
                                                                                                                                                                                                                                                                                                        23. .425
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                                                                                                                                                                                            Location/Qualifiers
                                                   61 ATKOAEAAAPVVESKWRAL 79
                                                                                                                                         Hepatitis C virus RNA helicase.
                                                                                                                                                                                                                                           (first entry)
 79; Conservative
                                                                                                                                                                             Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP06319583-A.
                                                                                                                           06-DEC-1995
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                                                                                                            AAR68864;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                            AAQ81559 encodes AAK68864 hepatitis C virus (HCV) RNA helicase. The DNA was used in the construction of an expression vector, which was used to transform a baculovirus host. The transformed baculovirus could then be used for the recombinant prodn. of HCV RNA helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SVVIVGRIILSGRPAVIPDREVLYQBFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                              of hepatitis C virus helicase gene in baculovirus - useful for large scale prodn. of RNA helicase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 394; DB 2; Length 3010; Best Local Similarity 100.0%; Pred. No. 5.6e-40; Matches 79; Conservative 0; Mismatches 0; Indels 0;
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/note= "partial proteinase; see AAR82692"
992. .1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "partial proteinase; see AAR82693"
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(SUMQ ) SUMITOMO METAL IND LTD.
(SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR82694 standard; protein; 3010 AA.
                                                                                                             (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1739 ATKQAEAAAPVVESKWRAL 1757
                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1-4; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATKQAEAAAPVVESKWRAL 79
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92JP-00325303.
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92JP-00249241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus; Virus.
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N-PSDB; AAT03960.
                                                                                                                                                                   WPI; 1995-040330/06.
N-PSDB; AAQ81559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3010 AA;
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The present sequence is a partial Hepatitis C Virus (HCV) polyprotein from the non-structral region. Partial proteinase sequences (AAR82692-93) are contained within this sequence. The proteinases can be used as anti-HCV agents. They can also be used to screen cpds. for their ability to inhibit their proteclytic activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)
                  An HCV proteinase active substance - which has activity as an anti-HCV agent and can be used to screen for proteinase inhibitors.
                                                                                                Disclosure; Page 39-48; 52pp; Japanese.
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Gaps .; 0 Query Match
Best Local Similarity 100.0%; Pred. No. 5.6e-40;
Matches 79; Conservative 0; Mismatches 0; Indels 0;

Sequence 3010 AA;

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Search completed: August 12, 2005, 14:14:59 Job time : 83.8821 secs

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US-08-324-977-32 US-08-384-616-32 US-08-904-686A-32 US-09-115-850-32 US-08-324-977-36 US-08-304-686A-36 US-08-304-686A-36 US-08-315-850-36 US-08-315-850-36 US-08-324-977-2 US-08-384-616-2 US-08-384-616-2 US-08-384-616-14 US-08-384-616-14 US-08-315-850-2 US-09-315-850-2 US-09-315-850-14 US-09-315-850-14 US-09-315-850-14

Sequence 36, Sequence 36, Sequence 36, Sequence 2, 1

Sequence Sequence Sequence Sequence Sequence 2, A Sequence 14, Sequence 2, A

Sequence Sequence Sequence

Sequence

ALIGNMENTS

Sequence

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August 12, 2005, 14:04:54; Search time 22.1278 Seconds (without alignments) 266.510 Million cell updates/sec
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Sequence 44,
Sequence 4, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                              1 SVVIVGRIILSGRPAVIPDR.....TATKQAEAAAPVVESKWRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-904-686A-44
US-09-315-850-44
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                          513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length
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Perfect score:
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| Sequence 44, Application US/08324977 |
| Patent No. 5747339 |
| GENERAL INFORMATION: |
| APPLICANT: OKAYAMA, Hiroto |
| APPLICANT: FUKE, Isao |
| APPLICANT: TAKAMIZAMA, Akahisa |
| APPLICANT: TAKAMIZAMA, Akahisa |
| APPLICANT: YOSHIDA, INA, NON-B HEPATITIS VIRUS GENOMIC |
| TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC |
| TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE |
| TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE |
| TOCKRESPONDENCE ADDRESS: |
| ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Naughton |
| CORRESPONDENCE ADDRESSEE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette, 3.5 in, 1.44Mb
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APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-077-1994
PRIOR APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: UF 2-167466
FILING DATE: 25-UN-1990
PRIOR APPLICATION NUMBER: UF 2-230921
FILING DATE: 31-AMC-1990
PRIOR APPLICATION NUMBER: UF 2-305605
FILING DATE: 09-WV-1990
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UUL-1993
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UUL-1993
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: STEVENS-SMICH, Theresa M.
REGISTRATION NUMBER: 36,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington
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US-08-324-977-44
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Appli Appl Appli

Sequence 16,

Sequence

Sequence Sequence

Sequence 2, Appl Sequence 9, Appl Sequence 16, App

JS-10-191-966-9 JS-10-191-966-16

Sequence 16,

Appli

Sequence Sequence Sequence

US-08-904-686A-12 US-09-315-850-12 US-08-952-981A-2 US-09-263-933-2

App]

Sequence Sequence Sequence

US-10-191-966-11 US-10-191-966-18 US-08-324-977-12 US-08-384-616-12

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Sequence

Sequence Sequence Sequence Sequence

Sequence 11, 1 Sequence 18, 1 Sequence 4, A

US-09-263-933-4 US-09-263-933-11 US-09-21-933-18 US-09-919-901-11 US-09-919-901-18 US-09-919-901-18

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FILING DATE: 01-AUG-1997
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APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
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FILING DATE: 02-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ATKQAEAAPVVESKWRAL 79
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
                                                                                            TELEX: 440142
INPORMATION POR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-384-616-44
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TOPOLOGY: linear
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APPLICANT: FUKE, Isao
APPLICANT: FUKE, Isao
APPLICANT: TRAKAMIZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: ONN-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: ONN-AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naudfhon
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                         Query Match 98.7%; Score 389; DB 1; Length 247; Best Local Similarity 96.2%; Pred. No. 1.4e-42; Matches 76; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
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APPLICATION NUMBER: US/08/384,616
FILING DATE:
CLASSIFECATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 25-0701-1991
APPLICATION NUMBER: UP 2-167466
FILING DATE: 25-0701-1990
PRIOR APPLICATION NUMBER: UP 2-30921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
AMME: SLEVENS-SMICH, Theresa M. REGISTRATION NUMBER: 36,281
    REFERENCE/DOCKET NUMBER: 900703D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             // Sequence 44, Application US/08384616
// Patent No. S847101
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 887-0357
TELEFAX: 440142
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ATKQAEAAPVVESKWRAL 79
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-08-324-977-44
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US-08-384-616-44
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64 SVVIVGRIILSGRPAIVPDRELLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 123
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                                                                                                                                       1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
                                                                     Gaps
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Patent No. 5998130

GENERALI INFORMATION:

APPLICANT: CKAYAMA, Hiroto

APPLICANT: TAKAMIZAMA, Haroto

APPLICANT: TAKAMIZAMA, Akahisa

APPLICANT: TAKAMIZAMA, Akahisa

APPLICANT: TAKAMIZAMA, Akahisa

APPLICANT: TAKAMIZAMA, NON-B HEBATITIS VIRUS GENOMIC

TITLE OF INVENTION: NON-A, NON-B HEBATITIS VIRUS GENOMIC

TITLE OF INVENTION: NON-A, NON-B HEBATITIS VIRUS GENOMIC

TITLE OF INVENTION: NON-A, NON-B HEBATITIS VIRUS GENOMIC

TITLE OF INVENTION: WESTER AND ANTIGEN POLYPEPTIDE

NUMBER OF SEQUENCES: 50

CORRESPONDENCES: 50

CORRESPONDENCES: A MESTER AND ANTIGEN MCLeland & ADDRESSER: NAUGHOON

STREET: 1725 K St. N.W. Suite 1000
Query Match 98.7%; Score 389; DB 2; Length 247; Best Local Similarity 96.2%; Pred. No. 1.4e-42; Matches 76; Conservative 3; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                     Length 247;
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APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chis ato
APPLICANT: MACHAZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: ONN-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.7%; Score 389; DB 2; Length 24 Best Local Similarity 96.2%; Pred. No. 1.4e-42; Matches 76; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US 08/324,977
                                     APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: McLeland, Le-Nunug
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELEFAN: (202) 69-2930
TELEFAN: (202) 69-2930
TELEFAN: (202) 69-2930
TELEFAN: (202) 697-0357
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
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APPLICATION NUMBER: US/09/315,850
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION DATE: 18-CL.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-167466
APPLICATION NUMBER: 25-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
PPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
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US-09-315-850-44
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Sequence 4, Application US/09263933

Factor No. 6280940

GENERAL INFORMATION:

APPLICANT: Potick, Amy K.

APPLICANT: Patick, Amy K.

TITLE OF INVENTION: BEDRERE GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT:

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT:

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

CURRENT APPLICATION NUMBER: 08/9263,933

CURRENT PILING DATE: 1999-03-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER APPLICATION DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTING DATE: 1998-08-05

SOFTWARE: PATENTING DATE: 1998-08-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.7%; Score 389; DB 3; Length 247; 96.2%; Pred. No. 1.4e-42; trive 3; Mismatches 0; Indel8
                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: MCLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REPERBNEK/DCCKET NUMBER: 900703G
TELECHOMINICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
INPORMATION FOR SEQ 1D NO: 44:
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1018 ATKOAEAAPVVESKWRAL 1036
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                                                                                        30-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 247 amino acids amino acid
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Best Local Similarity 96.2%
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-09-315-850-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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       Sequence 11, Application US/09263933
Fatent No. 6280940
GENURRAL INFORMATION:
GENURRAL INFORMATION:
APPLICANT: Potts, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER FILING DATE: 1999-08-05
SOFTWARE: PATENTING VIVE: 2.0
SEQ ID NO: 11
LENGTH: 1692
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Sequence 18, Application US/09263933

Patent No. 6280940

GENERAL INFORMATION:

APPLICANT: Potts, Karen E.

APPLICANT: Potts, Amy K.

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0006A

CURRENT PALICATION NUMBER: US/09/263,933

CURRENT PILING DATE: 1999-03-08

EARLIER APPLICATION NUMBER: 09/129,611

EARLIER PILING DATE: 1999-08-05

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      958 SVVIVGRIILSGRPAIVPDRELLYQEPDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.7%; Score 389; DB 3; 96.2%; Pred. No. 1.8e-41; iive 3; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 76; Conservative
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US-09-263-933-18
US-09-263-933-11
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Sequence 11, Application US/09919901

Patent No. 659978

GREREAL INFORMATION:
APPLICANT: Potts, Karen B.
APPLICANT: Potts, Karen B.
APPLICANT: Potts, Karen B.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REPRENCE: 0125-0005A
CURRENT FILING DATE: 2001-08-02
FRIOR PEPLING DATE: 1999-02-08-02
FRIOR PEPLING DATE: 1999-02-08-05
FRIOR PELING DATE: 1999-02-08-05
FRIOR PELING DATE: 1999-02-08-05
FRIOR PELING DATE: 1999-02-08-05
FRIOR PELING DATE: 1999-02-05-06-05
FRIOR PELING DATE: 1998-08-05
Sequence 4, Application US/09919901

Patent No. 6599738

GENERAL INFORMATION:
APPLICANT: Potts, Karen B.
APPLICANT: Potts, Karen B.
APPLICANT: Potts, Karen B.
APPLICANT: Potts, Raren B.
APPLICANT: Potts, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 1025-0005A
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR PLING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 4
LENGTH: 1692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.7%; Score 389; DB 4; Length 1692; 96.2%; Pred. No. 1.8e-41; tive 3; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 96.23
Best Local Similarity 76, Conservative
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SEQ ID NO 11
LENGTH: 1692
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US-10-191-966-18
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Sequence 4, Application US/10191966

Patent No. 6790612

GENERAL INFORMATION.

APPLICANT: Potts, Amy K.

TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE

FILE REFERENCE: 0125-0005A

CURRENT APPLICATION NUMBER: US/10/191,966

CURRENT APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: US/09/263,933

PRIOR APPLICATION NUMBER: 09/129,611

PRIOR PILING DATE: 1999-03-08

PRIOR PILING DATE: 1999-03-08
                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Potts, Karen E.
APPLICANT: Potts, Amy K.
APPLICANT: Patick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0.125-0005A
CURRENT APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1998-02-08
PRIOR FILING DATE: 1998-02-08
PRIOR FILING DATE: 1998-06-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 958 SVVIVGRIILSGRPAIVPDRELLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 1017
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18-05-919-901-18
; Sequence 18, Application US/09919901
; Patent No. 6599738
                                                                                   1018 ATKOAEAAPVVESKWRAL 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATKOAEAAAPVVESKWRAL 79
                                            61 ATKQAEAAAPVVESKWRAL 79
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Best Local Similarity 96.2%;
Matches 76; Conservative
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ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1692
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US-10-191-966-4
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US-10-191-966-4
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Sequence 18, Application US/10191966

| Patent No. 6790612
| Patent No. 6790612
| GENERAL INPORMATION:
| APPLICANT: Potts, Karen E.
| APPLICANT: Potts, Amy K.
| TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT ITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE CURRENT FILING DATE: 2002-07-10
| PRIOR APPLICATION NUMBER: US/10/191,966
| CURRENT APPLICATION NUMBER: US/09/263,933
| PRIOR FILING DATE: 1999-03-08
| PRIOR FILING DATE: 1999-03-08
| PRIOR FILING DATE: 1998-08-05
| NUMBER OF SEQ ID NOS: 33
| SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 958 SVVIVGRIILSGRPAIVPDRELLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 1017
                                                                                                                                 APPLICANT: Potts, Karen E.
APPLICANT: Potts, Karen E.
APPLICANT: Dackson, Roberta L.
APPLICANT: Patick, Amborta L.
APPLICANT: Patick, Amborta L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
CURRENT APPLICATION NUMBER: US/10/191,966
CURRENT PILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US/99/263,933
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR APPLICATION NUMBER: 1998-08-08
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
                                                                                                         1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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Pred. No. 1.8e-41;
3; Mismatches 0; Indels
     Length 1692;
                                                    Indels
  Score 389; DB 4;
Pred. No. 1.8e-41;
3; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/10191966; Patent No. 6790612; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 ATKOAEAAPVVESKWRAL 1036
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Sest Local Similarity 96.2%;
Matches 76; Conservative 3
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ORGANISM: Artificial Sequence
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Best Local Similarity 96.29
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: MACHAMIZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: CONA, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ASCII
SOFTWARE: ASCII
APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: B-OCT-1994
FILING DATE: B-OCT-1994
FILING DATE: B-OCT-1994
FILING DATE: B-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: J-AUG-1990
PRIOR APPLICATION NUMBER: JP 2-30605
FILING DATE: OS-NOV-1990
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: JO-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: OS-NOV-1990
PRIOR APPLICATION NUMBER: US 09/099,706
FILING DATE: OS-NOV-1990
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: OS-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1725 K St. N.W. Suite 1000 CITY: Washington STATE: D.C. STATE: U.S.A. ZIP: 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
                                                                                                                                                                                                                                                                                                                                                                                                                               1018 ATKQAEAAAPVVESKWRAL 1036
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Patent No. 5747339
                                                                                                                                                                                                                                                                                                                                                                                                      61 ATKQAEAAAPVVESKWRAL 79
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                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                  76; Conservative
                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                          OTHER INFORMATION:
SEQ ID NO 18
LENGTH: 1692
TYPE: PRT
                                                                                                                                                 US-10-191-966-18
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US-08-324-977-12
                                                                                                FEATURE:
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APPLICANT: FUKE, Isao
APPLICANT: FUKE, Isao
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITILE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITT' Washington
STATE: A
                                                                                                                                                                                          Ouery Match 98.7%; Score 389; DB 1; Length 2013; Best Local Similarity 96.2%; Pred. No. 2.2e-41; Matches 76; Conservative 3; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08384616; Patent No. 5847101; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     61 ATKQAEAAPVVESKWRAL 79
(202) 659-2930
(202) 887-0357
                            TELEX: 440142
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amino acids
                                                                                                                                    MOLECULE TYPE: protein US-08-324-977-12
                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-08-384-616-12
                   TELEFAX:
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us-09-758-308-3.rai
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0; Gaps
                                                                                Query Match 98.7%; Score 389; DB 2; Length 2013; Best Local Similarity 96.2%; Pred. No. 2.2e-41; Matches 76; Conservative 3; Mismatches 0; Indels 0
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Job time : 22.1278 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

August 12, 2005, 14:04:14; Search time 15.7224 Seconds (without alignments) 483.460 Million cell updates/sec Run on:

US-09-758-308-3 394 1 SVVIVGRIILSGRPAVIPDR......TATKQABAAAPVVESKWRAL 79 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Ouerv				
No.	Score	Match	Match Length	8	QI	Description
	394	100.0	3010	н	GNWVCJ	genome polyprotein
7	389	98.7	3010	-	GNWVTC	
٣	386	98.0	3010	7	A45573	
4	386	98.0	3010	-	GNWVTW	
Ŋ	385	7.76	3010	ч	S18030	
9	333	84.5	492	N	PS0326	n
7	332	84.3	3011	П	S40770	genome polyprotein
œ	328	83.2	3011	ч	GNWVC3	genome polyprotein
σ	324	82.2	3011	7	GNWVCH	
10	320	81.2	716	~	JQ1366	polyprotein - hepa
11	254	64.5	3014	-	JC5620	genome polyprotein
12	247	62.7	142	~	PC1307	
13	247	62.7	209	~	PC1306	genome polyprotein
14	229	56.1	876	~	PC2219	polypeptide - hepa
15	208	52.8	3033	Н	GNWVJ8	genome polyprotein
16	205	52.0	3033	Н	JQ1303	genome polyprotein
17	204	51.8	125	~	S35629	hypothetical prote
18	70.5	17.9	401	7	A89916	aspartokinase II (
19	67.5	17.1	980	7	871090	peroxisome biogene
20	64.5	16.4	286	~	G71899	hypothetical prote
21	64.5	16.4	483	~	E97255	transcription term
22	64	16.2	144	-	C70437	ATP synthase F0 su
23	64	16.2	1168	~	876195	hypothetical prote
	64	16.2	1697	~	T00079	hypothetical prote
25		16.1	278	~	T44412	ABC transporter (A
	63.5	16.1	423	~	AG1393	transcription term
27	63.5	16.1	423	~	AB1769	transcription term
28	•	16.1	446	N	A40896	Ca2+/calmodulin-de
59	63.5	16.1	1116	7	A84046	DNA polymerase III

쉽 8 g

methyl-accepting c	conserved hypothet	hypothetical prote	probable 6-deoxyer	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	probable pyruvate	alpha-actinin-4 -	hypothetical prote	hypothetical prote	ATP-dependent heli	GGDEF family prote	signal-transducing
D82077	T40832	A96791	T43231	AH2521	T19426	S31045	T16238	D71264	G71527	JC7186	D96746	AI1773	AD0412	E75292	B69435
0	N	~	7	~	~	~	~	7	~	~	~	~	~	7	0
433	688	808	3491	268	323	380	407	476	485	911	2777	215	828	856	908
16.0	16.0	16.0	16.0	15.9	15.9	15.9	15.9	15.9	15.7	15.7	15.7	15.6	15.6	15.6	15.6
63	63	63	63	62.5	62.5	62.5	62.5	62.5	62	62	62	61.5	61.5	61.5	61.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1
 GNWYCU GAWNCH DOLYDTOLEIN - hepatitis C virus (strain J) Sylontains: capsid protein C; envelope protein M; major envelope protein E; nonstructura protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus C;Bate: 30-Jun.1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
Riversaturi: M. 1923; F. 20000 Riversaturi: Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimot Dood Mari and cri fi s R7 9524.8528.3000
 A.Title: Molecular cloning of the human hepatitis C virus genome from Japanese patients A;Reference number: A39253; MUID:91088550; PMID:2175903
 A.Accession: A39253 A.Molecule type: genomic RNA
 Ajresidades: 1-3010 NANI. Ajressa references UNIPROT:P26662; GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g221611 B.K.to N. Orbesti C. Chimotopho V
Ajaco, No. Johnson 1, 30, 2012-2016, No. Proc. John. Acad. 65B, 219-223, 1989 A. TYETE: Japanese TSCIttes-64-the-non-A, non-B hepatitis viral genome show sequence vary
A. Reference number: PS0085
 A; Moleculani 2000 A; Roesidines 2650-2707 (KA2)
 A) Experimental source: Japanese isolate C. Comment: The cleavage sites of this polyprotein have not been determined.
C. Superfamily: hepatitis C virus genome polyprotein
C; Neywords: Air; glycopiocein; mydiolage; mucreolide binding; Frioly; polypiocein; seri: F;2-115/Product: capsid protein C #status predicted <cpc></cpc>
F;116-191/Product: envelope protein M #status predicted <bpm> F:192-389/Product: maior envelope protein E #status predicted <mee></mee></bpm>
 F;390-729/Product: nonstructural protein NS1 #status predicted <ns1></ns1>
 F;730-1006/Froduct: nonstructural protein NSZ #Status predicted <nsz> F;1007-1615/Product: hepacivirin #status predicted <nsz></nsz></nsz>
F;1230-1237/Region: nucleotide-binding motif A (P-loop) F;1312-1317/Region: nucleotide-binding motif B
 F.1516-1519/Region: DEAH MOCII F.1616-1862/Product: nonstructural protein NS4a #status predicted <n4a></n4a>
 F.1863-2013/Product: nonstructural protein NS4D #status predicted <n4b> F;2014-3010/Product: nonstructural protein NS5 #status predicted <ns5> F:196.209.234.250.305,325,417,423,430,448,532.556,576,623,645,1213,1255,2041,2077,2240,.</ns5></n4b>
Query Match 100.0%; Score 394; DB 1; Length 3010; Best Local Similarity 100.0%; Pred. No. 9.1e-34; Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 YTEOGRAFIE SCEDANIEDENT VORRERENEMENT PVTROGMOLAROFK

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61 ATKQAEAAAPVVESKWRAL 79
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Best Local Similarity 96.2%;
Matches 76; Conservative 2
                                                                                                                            Query Match
Best Local Similarity %0....
And 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A40244
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                                                                                                                  Cipecies: hepatitis C virus
A; Mori, C; Fuke, I:; Manabe, S:; Murakami, S.; Fujita, J.; Onishi, E.;
J. Virol. 65. 1105_1113, 1991
A; Takamizawa, A; Mori, C:; Fuke, I:; Manabe, S:; Murakami, S.; Fujita, J.; Onishi, E.;
J. Virol. 65. 1105_1113, 1991
A; Reference number: A38465; MulD:91140698; PMID:1847440
A; Recession: A38465; MulD:91140698; PMID:1847440
A; Reference number: A38465; MulD:91140698; PMID:1847440
A; Residues: 1-3010 c/TAX.
A; Residues: UNPROT:P26663; EMBL:M58335; NID:9329770; PIDN:AAA72945.1; PID:93297
C; Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstructural
C; Keywords: ATP; capsid protein C #status predicted c cEPM.
F; 116-191/Porduct: embelope protein M #status predicted c MSS.
F; 116-191/Porduct: nonstructural protein NS1 #status predicted c NS2.
F; 130-729/Porduct: nonstructural protein NS4 #status predicted c NS2.
F; 100-165/Product: nonstructural protein NS4 #status predicted c NS3.
F; 1116-1119/Region: nucleotide-binding motif B
F; 1116-1119/Region: DEXH motif
F; 11616-11862/Product: nonstructural protein NS4 #status predicted c NS3.
F; 1863-2013/Product: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Product: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Product: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Product: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Product: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Product: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Froduct: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Froduct: nonstructural protein NS5 *status predicted c NS3.
F; 1863-2013/Froduct: nonstructural protein NS5 *status predicted c NS3.
F; 
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A4573

946573

96000 polyprotein - hepatitis C virus (strain JT)

96000 protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C;Species: hepatitis C virus

C;Species: hepatitis C virus

C;Species: hepatitis C virus

C;Accession: A45573

R;Tanaka, T: Kato, N: Nakagawa, M: Octsuyama, Y:; Cho, M.J.; Nakazawa, T:; Hijikata, Virus Res. 23, 39-53, 1992

A;Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: B

A;Reference number: A45573

A;Status: preliminary

A;Residues: preliminary

A;Residues: preliminary

A;Residues: L-3010 < TAN>

A;Cross-references: UNLROCT: 000269; GB:D11168; GB:D01171; NID:g221612; PIDN:BAA01943.1;

A;Everimental source: HCV-JT

A;Residues: ATP; GIVCOPOCIEN (C virus genome polyprotein

C;Superfamily: hepatitis C virus genome polyprotein

C;S
genome polyprotein – hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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A, Molecule type: genomic RNA
A, Residues: 1-3010 cCHES
A, Rossidues: 1-3010 cCHES
A, Residues: 1-3010 cCHES
A, Residues: 1-3010 cCHES
A, Residues: 1-3010 cCHES
C, Superfamily: hepatistic C virus genome polyprotein
C, Superfamily: hepatistic C virus genome polyprotein; glycoprotein; hydrolase; nonstructura
C, Superfamily: hepatistic C virus genome polyprotein; glycoprotein; hydrolase; nonstructura
F;116-191/Product: capelope protein M #status predicted cEPM>
F;130-139/Product: nonstructural protein NS1 #status predicted cNS1>
F;390-729/Product: nonstructural protein NS2 #status predicted cNS2>
F;1007-1615/Product: hepacivirin #status predicted cNS2>
F;1007-1615/Product: noncleotide-binding motif B
F;1312-1317/Region: nucleotide-binding motif B
F;1312-1317/Region: nucleotide-binding motif B
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F;1863-2013/Product: nonstructural protein NG4b #status predicted <N4B>
F;2014-1010/Product: nonstructural protein NG5 #status predicted <NGS>
F;2014-2010,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,207
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N. Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS4a; nonstructural protein NS4a; nonstructural protein C, Species: hepatitis C virus
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R;Chen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
R;Chen, P.J.; Lin, M.H.; 1992
189, 188, 102-113, 1992
A;Title: The Taiwanese hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92230206; PMID:1314449
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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                                                                                                                       Fill6-1119/Region: DEXH motif
Fil62-1682/Product: nonstructural protein NS4a #status predicted <N4A>
Fil683-2013/Product: nonstructural protein NS4b #status predicted <N4B>
Fil014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
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Pred. No. 6.6e-33;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                          Length 3010;
                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
F;1007-1615/Product: hepacivirin #status predicted <NS3
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1312-1317/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                      Score 386; DB 1;
Pred. No. 6.6e-33;
3; Mismatches 0;
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), Contains: capsid protein C, envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS4s; nonstructural protein NS4s; nonstructural protein NS4s; nonstructural protein NS5
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R; Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda,
Jpn. J. Exp. Med. 60, 167-177, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: D00831; NID: g221511; PIDN: BAA00705.1; PID: g221512
A; Experimental source: isolate HC-J1
A; Experimental source: isolate HC-J1
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Superfamily: hepatitis C virus genome polyprotein
C; Reywords: ATP: g1ycoprotein; hydrolase; mucleotide binding; P-loop; polyprotein; er.
F; 116-191/Product: capsid protein M #status predicted <PEM>
F; 116-191/Product: major envelope protein B #status predicted <NES>
F; 390-729/Product: nonstructural protein NSI #status predicted <NSI>
F; 730-1006/Product: nonstructural protein NSI #status predicted <NSI>
F; 116-151/Region: nucleotide-binding motif A (P-loop)
F; 1312-1317/Region: nucleotide-binding motif B
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstruct)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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                                                                                                                                                                                       C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004 C;Accession: S40770; PC1285 R;Okamoto, H. submitted to the EMBL Data Library, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          revision 30-Sep-1992 #text_change 09-Jul-2004
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B:
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Length 492;
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   Score 333; DB 2;
Pred. No. 4.7e-28;
9; Mismatches 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S40770
A;Reference number: S40770
A;Accession: S40770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome polyprotein - hepatitis C virus N; Contains: capsid protein C; envelope
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                                                                                                                                                                                                                                                                                                                                                 S91 SRQAEAITPAVQTNWQRL 308
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C.Date: 30-Sep-1992 #sequence revis:
C.Accession: A39166; PQ0403; PQ0404
                                                                                                                                                                                                                                                                                                      79
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       84.5%;
79.5%;
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                                                                                                                                                                                                                                                                                                      62 TKOAEAAAPVVESKWRAL
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                                                                                    62; Conservative
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A; Residues: 1-513 < OK2>
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: PS6326
R;Li, J.S.; Tong, S.P.; Vitvitski, L.; Lepot, D.; Trepo, C.
Gene 105, 167-172, 1991
A;Title: Two French genotypes of hepatitis C virus: homology of the predominant genotype
A;Reference number: PS0326
A;Accession: PS0326
A;Accession: PS0326
A;Molecule type: genomic RNA
A;Residues: 1-492 <LIJ>A;Cross-references: UNIPROT:Q9IFE5; UNIPROT:036579; UNIPROT:036610; UNIPROT:Q03463; UNIPROT:Cost-this sequence corresponds to nonstructural protein NS3 region
A;Note: translation of the nucleotide sequence is not complete
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Argen. virol. 128, 129.169, 1993
Argenence analysis of putative structural regions of hepatitis C virus isolated A;Reference number: A48332; MUID:93119270; PMID:8380322
A;Recession: 833570
A;Accession: 82570
A;Accession: 
       A; Variety: isolate JK1
C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C; Accession: S18030; S33570; A48332; S18029
R; Honda, M.; Kaneko, S.; Massahi, U.; Kobayashi, K.; Murakami, S.
submitted to the EMBL Data Library, September 1991
A; Description: A whole genome of hepatitis C virus cDNA was isolated from a single patie
A; Accession: S18030
A; Molecule type: genomic RNA
A; Residues: 1-3010 <HON>
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:068949; EMBL:X61596; NID:959478; PIDN:CAA43793.1; PID:959479
A;Experimental source: isolate JK1 from an individual
A;Experimental source: isolate JK1 from an individual
A;Fhonda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. Virol. 128, 163-169, 1993
A;Title: Sequence analysis of putative structural regions of hepatitis C virus isolated
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Pred. No. 8.5e-33;
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genome polyprotein - hepatitis C virus (strain H)
N;Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
D;Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A38814; A41546
R;Inchauspe, G; Zebedee, S; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
submitted to GenBank, July 1992
A;Description: Genomic structure of the human prototype strain H of hepatitis C virus: G
A;Reference number: A36814
A;Accession: A38814
A;Accession: A38814
A;Molecule type: genomic RNA
A;References: UNIPROT:P27958; GB:M67463; NID:G329737; PIDN:AAA45534.1; PID:G329738
B;Inchauspe, G; Zebedee, S; Lee, D.H.; Sugitani, M.; Nasoff, M.; Prince, A.M.
Proc: Natl. Acad. Sci. U.S.A. 88; 10292-102956, 1991
A;Title: Genomic structure of the human prototype strain H of hepatitis C virus: comparil A;Reference number: A41546; MUID:92052256; PMID:1658800
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83.2%; Score 328; DB 1; Lengta. -. Pred. No. 1.2e-26; Indels
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Matches 60; Conservative
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A;Note: neither amino acid nor nucleotide sequence is given C;Superfamily: hepatitis C virus genome polyprotein (5.Keywords). ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructura (5.Keywords). ATP; capsid protein C #status predicted <CPC> F;116-191/Product: capsid protein C #status predicted <CPC> F;115-191/Product: major envelope protein B #status predicted <MEE> F;192-389/Product: major envelope protein NS1 #status predicted <NS1> F;300-1006/Product: nonstructural protein NS2 #status predicted <NS1> F;120-1137/Region: nucleotide-binding motif A (P-loop) F;1317/Region: nucleotide-binding motif B (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fil616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
Fil616-13013/Product: nonstructural protein NS4b #status predicted <N4B>
Fil014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
Fil014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
Fil05,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
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C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: JQ1366
R;Kremsdorf, D.; Porchon, C.; Kim, J.P.; Reyes, G.R.; Brechot, C.
J. Gen. Virol. 72, 2557-2561, 1991
A;Title: Partial nucleotide sequence analysis of a French hepatitis C virus: implication A;Reference number: JQ1366
A;Accession: JQ1367
A;A
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Acamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
A;Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant
A;Reference number: JC5620; MUID:97366593; PMID:9223423
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98)
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 VVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQTA
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Csuperfamily: hepatitis C virus genome polyprotein
C;Keywords: glycoprotein; polyprotein
F;84,90,97,115,143,199,223,245,290,312/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3011;
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75.6%; Pred. No. 1.8e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.2%; Score 324; DB 1;
76.9%; Pred. No. 3.1e-26;
iive 9; Mismatches 9
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689 SRQAEVITPAVQTNWQRL 706
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hes 60; Conservative
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A; Residues: 1-716 < KRE>
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45; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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A; Molecule type: mRNA
A; Residues: 1-3014 <CIRA>
A; Residues: 1-3014 <CIRA>
A; Residues: 1-3014 <CIRA>
A; Croses references: UNIPROT: 039928; GB: Y13184
A; Experimental source: genotype 5a, which predominates in South Africa
A; Note: the translation of the nucleotide sequence is not complete in this paper
C; Superfamily: hepatitis C virus genome polyprocetin
F; 2-115/Product: capsid procetin C #status predicted <CRE>
F; 196-19/Product: major envelope protein B #status predicted <NSI>
F; 334-408/Region: hypervariable #status predicted <NSI>
F; 331-1007/Product: nonstructural protein NSI #status predicted <NSI>
F; 131-1238/Region: nucleotide-binding motif A (P-loop)
F; 1313-1318/Region: nucleotide-binding motif B
F; 1313-1318/Region: nucleotide-binding motif B
F; 1313-1318/Region: DEXH motif
C; Nordator Complement Compl
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C;Species: hepatitis C virus
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: PC1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome polyprotein NS4a epitope containing region (isolate HD10-1) - hepatitis C virus C;Species: hepatitis C virus C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C;Accession: PC1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C; Accession: PC1307
R; Sturyver, L., ivan Arnhem, W; Wyseur, A; DeLeys, R.; Maertens, G.
Biochem. Biophys. Res. Commun. 192, 635-641, 1993
A; Title: Analysis of the putative El envelope and NS4a epitope regions of HCV type 3. A; Reterence number: PC1300; MUID:93249436; PMID:7683463
A; Accession: PC1307
A; Molecule type: mRNA
A; Accession: PC1307
A; Molecule type: mRNA
A; Cross-references: UNIPPCT:Q68870; DDBJ:D14602
A; Experimental source: blood
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: polyprotein
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64.5%; Score 254; DB 1; Length 3014;
Best Local Similarity 61.8%; Pred. No. 1.1e-18;
Matches 47; Conservative 12; Mismatches 17; Indels
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59.0%; Pred. No. 2.2e-19;
tive 12; Mismatches 20;
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Best Local Similarity
Matches 46; Conserva
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R;Stuyver, L.; Van Arnhem, W.; Wyseur, A.; DeLeys, R.; Maertens, G.
Biochem. Biophys. Res. Commun. 192, 635-641, 1993
A;Title: Analysis of the putative El envelope and NS4a epitope regions of HCV type 3.
A;Reference number: PC1306
A;Accession: PC1306
A;Accession: PC306
A;Residues: 1-209 <STUJA
A;Residues: 1-209 <STUJA
A;Cross-references: UNIPROT:Q81594; DDBJ:D14600; NID:g303584; PIDN:BAA03449.1; PID:g3035
A;Cross-references: UNIPROT:Q81594; DDBJ:D14600; NID:g303584; PIDN:BAA03449.1; PID:g3035
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: nonstructural protein; polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide - hepatitis C virus (type 5a) (fragments)
NSA proteins core protein; El (carboxyl end); E2/NS1 (amino end); NS3 protein; NSAA proteins; Species; hepatitis C virus
C; Date: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E2, and NS3/NS4 regions of the 1
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N/Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstruct
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
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A;Residues: 1-876 <STU>
A;Cross-references: UNIPROT:Q81242; GB:L29577; GB:L29579
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; Pred. No. 1.4e-16;
13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                   62.7%; Score 247; DB 2; Length 20
57.7%; Pred. No. 3.4e-19;
ive 13; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Stuyver, L.; Arnhem, W.V.; Wyseur, A.; Maertens, G. Biochem. Biophys. Res. Commun. 202, 1308-1314, 1994 A;Title: Cloning and phylogenetic analysis of the core, A;Reference number: PC2219; MUID:94338342; PMID:7520237 A;Accession: PC2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A, Experimental source: serum
C, Superfamily: hepatitis C virus genome polyprotein
C, Keywords: protein
F;1-191/Product: core #status predicted <COE>
F;68-78/Region: variable
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F;412-783/Product: NS3 #status predicted <NSR>
F;784-337/Product: NS4A #status predicted <NSR>
F;888-87/Fyroduct: NS4B #status predicted <NSB>
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Best Local Similarity 60.0%;
Matches 42; Conservative 13
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Best Local Similarity 50.0%; Pred. No. 9.5e-14;
Matches 39; Conservative 14; Mismatches 25; Indels 0; Gaps
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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POLG HCVBK
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2: uniprot_trembl:*
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_	Q9qp61 hepatitis c	_	Q68216 hepatitis c	_	_	_	Q68228 hepatitis c	Q68k50 hepatitis c	_	Q807p3 hepatitis c	Q9dtf0 hepatitis c	Q9j3g5 hepatitis c	Q9j3h0 hepatitis c
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389	389	389	388	388	387	387	387	387	387	387	387	387	387

## ALIGNMENTS

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PEROLOGICAL CONTRIBUTION OF STANDARD; PRT; 3010 AA.

DE 26662.

TO 1-M02-1992 (Rel: 23, Last sequence update)

TO 25-6CT-2004 (Rel: 45, Last annotation update)

TO 1-M02-1992 (Rel: 23, Last sequence update)

TO 1-M02-1992 (Rel: 35, Last sequence update)

TO 1-M02-1992 (Rel: 45, Last annotation update)

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SEQUENCE
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NITEETERO IPRO02521 HCV_core.

NITEETERO IPRO02531 HCV_NS4D.

NITEETERO IPRO02661 HCV_NS4D.

NITEETERO IPRO02666 HCV_NS2D.

NITEETERO IPRO02666 HCV_CORE I.

NETERO PEOLISS HCV_core I.

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NETERO PEOLISS HCV_NS2 I.

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NETERO PEOLI
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Capsid protein C (Potential).
Matrix protein (Potential).
Major envelope protein B (Potential).
Nonstructural protein NS1 (Potential).
Nonstructural protein NS2 (Potential).
Protease/helicase NS3 (Potential).
Nonstructural protein NS4 (Potential).
Nonstructural protein NS4B (Potential).
Nonstructural protein NS4B (Potential).
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ATP (Potential).
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     send an email to license@isb-sib.ch).
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PIR; A39253; GWWCJ.
HSSP; P26663; 1JXP.
MEROPS; S29.001; --
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A Aizaki H., Aoki Y., Harada T., Ishii K., Suzuki T., Nagamori S.,
Aizaki H., Aoki Y., Harada T., Ishii K., Suzuki T., Nagamori S.,
Toda G., Matesuura Y., Miyamura T.;
Infectious blood sample.";
Inferpro; IPRO01410; DRAD.
Interpro; IPRO01521; HCV_core.
Interpro; IPRO01521; HCV_core.
Interpro; IPRO01521; HCV_NASA.
Interpro; IPRO01521; HCV_NASA.
Interpro; IPRO01521; HCV_NASA.
Interpro; IPRO01521; HCV_NASA.
Interpro; IPRO01531; HCV_NASA.
Interpro; IPRO01531; HCV_NASA.
Interpro; IPRO01531; HCV_NASA.
Interpro; IPRO01531; HCV_NASA.
Interpro; IPRO01540; HCV_NASA.
Interpro; IPRO01551; HCV_NASA.
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Hepacivirus.
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                                                        100.0%; Score 394; DB 1; Length 3010; 100.0%; Pred. No. 4.1e-32;
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3010 AA; 327017 MW; AA993794F46DB185 CRC64;
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Last sequence update)
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InterPro; IPR0012166; HCV_NSS3.
InterPro; IPR00105166; Helicase_C.
InterPro; IPR0014109; Peptidase_S29.
InterPro; IPR00103; Pept_Sar_Cys.
InterPro; IPR00103; Pept_Sar_Cys.
InterPro; IPR001095; RNA_Pol_DS_PS.
InterPro; IPR007095; RNA_Pol_DS_PS.
InterPro; IPR011034; HCV_Copsid; 1.
Pfam; PP01542; HCV_Core; 1.
                                                                                                                                                                                                                                                                                                                                                       1739 ATKQAEAAAPVVESKWRAL 1757
                                                                                                                                                                                                                                                                                                                  61 ATKOAEAAAPUVESKWRAL 79
                                                           Query Match
Best Local Similarity 100.0%;
Matches 79; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein.
Hepatitis C virus.
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1679 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT 1738
                                                                                                                                                                                                                                                                                                                                                 DR PEam; PF01538; HCV_NS1; 1.

DR Pfam; PF01538; HCV_NS2; 1.

DR Pfam; PF01001; HCV_NS3; 1.

DR Pfam; PF01001; HCV_NS4s; 1.

DR Pfam; PF01001; HCV_NS4s; 1.

DR Pfam; PF00298; Viral_RGP; 1.

DR Pfam; PF00998; Viral_RGRP; 1.

DR SWART; SN00487; DSXDC; 1.

DR Pfam; PF00190; CYTOCHROME_C; UNKNOWN_1.

KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; KW Polyprotein; Transmembrane.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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SEQUENCE FROM N.A.
MEDLINE=95186115; PubMed=7765873; DOI=10.1016/0168-1656(94)00134-X;
Seki M., Honda Y., Kondo J., Pukuda K., Ohta K., Sugimoto J.,
Yamada E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Effective production of the hepatitis C virus core antigen having high purity in Eschericia coli."; J. Biotechnol. 38:229-241(1995).

EMBL; D30613; BAA06303.1; -.
PIR; A61196; A61196.
PIR; P00246; P00246.
PIR; P80329; PS0329.
HSSP; Q81755; 1DXP.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0003968; F:NAA-directed RNA polymerase activity; IEA.
GO; GO:000368; F:NAA-directed RNA polymerase activity; IEA.
GO; GO:0008236; F:Serine-type peptidase activity; IEA.
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UNOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 4.1e-32;
iive 0; Mismatches 0;
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                                                                                                     InterPro; IRRN01650; Helicase C.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR005003; Pept Ser Cys.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007094; RNA pol DS PS.
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Ouery Match

Best Local Similarity 100.v.,

Best Local Similarity 100.v.,
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Pfam; PF01542; HCV core; 1.
Pfam; PF01539; HCV env; 1.
Pfam; PF01560; HCV NS1; 1.
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                                                                                  nterPro;
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                                                                                                               Pfam; PP01006; HCV_NS4s; 1.
Pfam; PP01006; HCV_NS4s; 1.
Pfam; PP01001; HCV_NS4s; 1.
Pfam; PF00771; Helicase 2.
Pfam; PF00798; Viral RdRP; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; SP0190; CASS 2.
SEQUENCE 3010 AA; 327352 MW; 888BBA102A733390 CRC64;
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Hepacivirus.
NCBI_TaxID=11103;
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MEDILINE-96362188; PubMed-8720135;
Sexi M., Honda Y.;
"Phosphorothioate antisense oligodeoxynucleotides capable of inhibiting hepatitis C virus gene expression: in vitro translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:0019028; C:viral capsid; IEA.

R GO; GO:00019021; C:viral envelope; IEA.

R GO; GO:00019028; C:viral envelope; IEA.

R GO; GO:00019028; F:ATP-dependent helicase activity; IEA.

R GO; GO:00019028; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0001908; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0001908; F:RT:ne-type peptidase activity; IEA.

R GO; GO:0001908; F:Structural molecule activity; IEA.

R GO; GO:0005198; F:Structural genome replication; IEA.

R GO; GO:00019087; P:viral genome replication; IEA.

R GO; GO:0019087; P:viral genome replication; IEA.

R INTERFO: IPR001410; DEAD.

R INTERFO: IPR001522; HCV_capsid.

R INTERFO: IPR002521; HCV_capsid.

R INTERFO: IPR002511; HCV_ene.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Hepatitis C virus.
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Pfam;
Pfam;
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Hepacivirus.
NCBI_TaxID=11103;
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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Hepacivirus.
NCBI_TaxID=11103;
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Yao X., Guo J., Zheng C.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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GO:0005198, F:structural molecule activity; IEA. GO:0006508; P:proteolysis and peptidolysis; IEA. GO:0006350, P:transcription; IEA. GO:019079; P:viral genome replication; IEA. GO:0119087; P:viral transformation; IEA.
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0-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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InterPro; IPR004169; Helicase_C.
InterPro; IPR004109; Peptidase_S29.
InterPro; IPR004109; Peptidase_S29.
InterPro; IPR004109; Peptidase_S29.
InterPro; IPR007099; RNA_POI_PS PG
InterPro; IPR007099; HCV_CORE; I.
Pfam; PF01539; HCV_CORE; I.
Pfam; PF01539; HCV_NS2; I.
Pfam; PF01001; HCV_NS4; I.
Pfam; PF01001; HCV_NS4b; I.
  GO; GO:0005198; F:structural molecui
GO; GO:0006508; P:proteolysis and pr
GO; GO:0006350; P:transcription; IE
GO; GO:0019079; P:viral genome repl:
GO; GO:0019079; P:viral transformat:
InterPro; IPR000345; CYtC_heme_BS.
InterPro; IPR001410; DEAD.
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InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
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                                                                                                                                                                                                                                                                                  HCV env.
HCV NS1.
HCV NS4a.
HCV NS4b.
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Hepatitis C virus.
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InterPro; IPR000745;
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InterPro; IPR002868;
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1679 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGWQLAEQFKQKALGLLQT 1738
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SMART; SM00487; DEXDG; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON TER 3013 3013
SEQÜENCE 3013 AA; 327180 MW; C71FA2B7C5257F3D CRC64;
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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0
Moser, Co. 1001601, C. integral to membrane; IEA.

GO; GO:0019028; C. viral capsid; IEA.

GO; GO:0019029; C. viral capsid; IEA.

GO; GO:00019029; F. ATP binding; IEA.

GO; GO:0008026; F. ATP dependent helicase activity; IEA.

GO; GO:0008123; F. RNA-directed RNA polymerase activity; IEA.

GO; GO:0008126; F. STRIP binding; IEA.

GO; GO:0008126; F. STRIP binding; IEA.

GO; GO:0008126; F. STRIP binding; IEA.

GO; GO:000818; F. STRIP binding; IEA.

GO; GO:000818; F. STRIP binding; IEA.

GO; GO:0008199; P. STRIP STRIP molecule activity; IEA.

GO; GO:0008199; P. STRIP STRIP peptidolysis; IEA.

GO; GO:0008199; P. STRIP STRIP STRIP STRIP STRIP.

GO; GO:0008199; P. STRIP STRIP STRIP STRIP STRIP.

GO; GO:0019087; P. VINTAL GENOME FEDICATION; IEA.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3013 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR009003; Pept_Ser_Cys.
InterPro; IPR002518; Pept_039_HCV NS2.
InterPro; IPR0070995; RNA_DOl_DS_PS.
InterPro; IPR0070994; RNA_DOl_PSvir.
   GO; GO: 0016021; C: integral to membra GO; GO: 0019028; C: viral capsid; IEA. GO; GO: 0019029; C: viral capsid; IEA. GO; GO: 0019021; C: viral envelope; IEA. GO; GO: 0005524; F: ATP-dependent heli GO; GO: 000326; F: ATP-dependent heli GO; GO: 000326; F: RNA- binding; IEA. GO; GO: 000326; F: RNA- binding; IEA. GO; GO: 0005198; F: RNA-directed RNA GO; GO: 00065198; F: RNA-directed RNA GO; GO: 00065198; P: proteclysis and ped GO; GO: 00065199; P: proteclysis and ped GO; GO: 0019079; P: viral genome repli GO; GO: 0019087; P: viral genome repli InterPro; IPR001410; DEAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEAD/DEAH N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ATKQAEAAAPVVESKWRAL 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR001650, Helicase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00271; Helicase C; 1
Pfam; PF00998; Viral RdRP; 1
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01543; HCV capsid;
Pfam; PF01542; HCV core; 1.
Pfam; PF01539; HCV env; 1.
Pfam; PF01560; HCV NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01506; HCV_NS5a; 1
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nes 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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61 ATKOAEAAAPUVESKWRAL 79
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                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=11103;
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01-MAY-2000
01-MAY-2000
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                                                        MEDLINE=20013325; PubMed=10544098; DOI=10.1006/viro.1999.9924; Nagayama K., Kuroeshii, Enomoto N., Maekawa S.y., Miyasaka Y., Tazawa J.i., Izumi N., Marumo F., Sato C.; Tazawa J.i., Izumi N., Marumo F., Sato C.; Tratade denanges in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Nonstructural protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:001601; C:integral to membrane; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019029; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope. IEA.
GO; GO:0008026; F:ATP binding; IEA.
GO; GO:0003723; F:RN-dependent helicase activity; IEA.
GO; GO:0003526; F:RN-dependent helicase activity; IEA.
GO; GO:0000356; F:RN-directed RNA polymerase activity; IEA.
GO; GO:00005198; F:structural molecule activity; IEA.
GO; GO:0005508; P:structural molecule activity; IEA.
GO; GO:0005508; P:proteolyais and peptidolyais; IEA.
GO; GO:0005509; P:viral genome replication; IEA.
GO; GO:0019087; P:viral transformation; IEA.
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Coat protein; Envelope protein; Glycoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR004109; Peptidase S29.
InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR002518; Pept W39 HCV NS2.
InterPro; IPR007099; RNA_pol_DS_FS.
InterPro; IPR0070094; RNA_pol_DS_FS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV capsid.
InterPro; IPR002531; HCV cnr.
InterPro; IPR002531; HCV NS1.
InterPro; IPR001495; HCV NS4a.
InterPro; IPR001496; HCV NS4b.
InterPro; IPR002868; HCV NS4b.
InterPro; IPR002866; HCV RdRP.
InterPro; IPR00166; Helicase C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000345; Cytc heme_BS.
InterPro; IPR001410; DEAD.
InterPro; IPR011545; DEAD/DEAH_N.
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Pfam; PF01538; HCV_NS2; 1.
Pfam; PF0290; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4b; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00271; Hellcase_C; 1.
Pfam; PF00598; Viral_RGRP; 1.
                                                                                                                                                                                         Virology 263:244-253(1999).
EMBL; AF165056; AAD56191.1; -.
PIR; A61196; A61196.
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     SEQUENCE FROM N.A.
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53 SVVIVGRIILSGRPAIIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIJNE=95146953; PubMed=7844535;
Greene W.K., Cheong M.K., Ng V., Yap K.W.;
"Prevalence of hepatitis C virus sequence variants in South-East
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                         068217;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNOV-1996 (TrEMBLrel. 24, Last annotation update)
Nonstructural protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 3013 AA.
                                                                                                                       138 AA
                                                                                                                       PRT;
1742 ATKQAEAAAPVVESKWRAL 1760
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EMBL; U14253; AAC53942.1; -.
HSSP; P26663; 1CU1.
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InterPro; IPR000745; HCV NS4a.
InterPro; IPR001490; HCV NS4b.
Pfam; PF01006; HCV NS4b; 1.
Pfam; PF01001; HCV_NS4b; 1.
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Virology 263:244-253(1999).
EMBL; AF165055; AAD56190.1; -.
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                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nonstructural protein.
NON TER 1 1 1 1 NON TER 138 138 SEQUENCE 138 AA; 151
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1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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InterPro;
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InterPro;
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InterPro;
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InterPro;
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Cost protein; Envelope protein; Glycoprotein; Nonstructural protein;
Pelyprotein; Transmembrane, 762E2D4B6B607B8C CRC64;
SEQUENCE 3013 AA; 326887 MW; 762E2D4B6B607B8C CRC64;
                                                                                                                                                                                                        R GO; GO: 0015021; C: integral to membrane; IEA.
R GO; GO: 0019028; C: viral capsid; IEA.
R GO; GO: 0019021; C: viral capsid; IEA.
R GO; GO: 00019021; C: viral capsid; IEA.
R GO; GO: 0005125; F: RATP-dependent helicase activity; IEA.
R GO; GO: 00003725; F: RATP-dependent helicase activity; IEA.
R GO; GO: 00003126; F: RATP-dependent helicase activity; IEA.
R GO; GO: 00005136; F: Retructural molecule activity; IEA.
R GO; GO: 00005136; F: serine-type peptidase activity; IEA.
R GO; GO: 00005136; F: seructural molecule activity; IEA.
R GO; GO: 00005136; P: proceolysis and peptidolysis; IEA.
R GO; GO: 0019007; P: viral genome replication; IEA.
R GO; GO: 0019007; P: viral genome replication; IEA.
R GO: GO: 0019007; P: viral transformation; IEA.
R InterPro; IPR0004416; DEA.
R InterPro; IPR0004416; DEA.
R InterPro; IRR004410; DEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 99.7%; Score 393; DB 2; Local Similarity 98.7%; Pred. No. 5.3e-32; Des 78; Conservative 1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptidase S29.
Pept Ser Cys.
Pept U39 HCV NS?
RNA DOI DS PS.
RNA DOI PSVIr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1742 ATKOAEAAPVVESKWRAL 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR011545; DEAD/DEAH N. InterPro; IPR002522; HCV_capsid. InterPro; IPR002521; HCV_core. InterPro; IPR002519; HCV_ene. InterPro; IPR002511; HCV_NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ATKOAEAAPVVESKWRAL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01000; MCV NS43; 1.
Pfam; PF01001; HCV NS48; 1.
Pfam; PF01001; HCV NS58; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF00398; Viral RdRP; 1.
SMART; SMO487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF01543; HCV capaid, Pfam, PF01542; HCV core; 1. Pfam, PF01539; HCV env; 1. Pfam; PF01560; HCV NS1; 1. Pfam; PF01594; HCV NS3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nterPro; IPR007094; RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                       PIR, PQ0254; PQ0254.
PIR, PQ0804; PQ0804.
PIR, PS0329; PS0329.
HSSP; Q8JYS1; 1CWX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001490;
                                  PIR; PQ0246;
PIR; PQ0251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; Il
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Matches
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Q9DTES
ID Q9DTI
AC Q9DTI
DT 01-M
DT 01-M
   SOW WAS A WALL OF THE WALL OF 
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Mishiro S.;
Mishir
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Polyprotein; Transmembrane.
SEQUENCE 3010 AA; 326987 MW; 573C0F3C55B3F3F4 CRC64;
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                   TISSUE-Serum;
Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004109; Peptidase S29.
InterPro; IPR005003; Pept Ser Cys.
InterPro; IPR007518; Pept U39 HCV NS2.
InterPro; IPR0070095; RNA pol DS PS.
InterPro; IPR007094; RNA pol DS PS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000345; CytC heme BS.
InterPro; IPR011410; DEAD.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV RdRP.
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Pfam; PF01542; HCV_core; 1.
Pfam; PF01550; HCV_NS1; 1.
Pfam; PF01560; HCV_NS1; 1.
Pfam; PF02907; HCV_NS3; 1.
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Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF00998; Viral RGRP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002531;
IPR000745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .PR001650;
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                  NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01006; H
Pfam; PF01001; H
Pfam; PF01506; H
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Query Match
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                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                           Mushino S.;

Mith hepatities C virus (HCV) genotype lb sequences from fifteen patients
with hepatocellular carcinoma: the 'progression score' revisited.";

MEMBL; AB049093; BAB1806.1; -.

BRB1; A00149; P00246.

BRB1; P00246; P00246.

BRR; P00246; P00246.

BRR; P00246; P00246.

BRR; P00046; P00246.

BRR; P00046; P00246.

BRR; P00046; P00246.

BRR; P00046; P00246.

BRR; P00040; PRR; P00246.

BRR; P00040; PRR; P00246.

BRR; P00040; PRR; P00246.

BRR; P0000524; FrRY binding; LBA.

GO; GO:0003722; FrRY binding; LBA.

GO; GO:0003723; FrRY binding; LBA.

GO; GO:000368; FrRY binding; LBA.

GO; GO:000368; FrRY binding; LBA.

GO; GO:000368; FrEYT binding; LBA.

GO; GO:000368; FrEY binding; LBA.

INTERPOR; PRR00145; HCV. GAPB;

INTERPOR; PRR00146; HCV. NS4A.

INTERPOR; PRR00146; HCV. NS4A.

INTERPOR; PRR00166; HCV. NS4A.
                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
                                                                                                                                                                                                                                                                                            Takahashi K., Iwata K., Matsumoto M., Matsumoto H., Nakao K.,
Hatahara T., Ohta Y., Kanai K., Maruo H., Baba K., Hijikata M.,
                                                                                                                                           | MAR-2001 (TrEMBLrel. 16, Created)
|-MAR-2001 (TrEMBLrel. 16, Last sequence update)
|-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                    PRT; 3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004109; Peptidase 529.
InterPro; IPR009003; Pept Ser Cys.
InterPro; IPR002518; Pept U39 HCV NS2.
InterPro; IPR007095; RNA DO1 DS PS.
InterPro; IPR007094; RNA DO1 PSVIr.
                                                 1739 ATKOAEAAPVVESKWRAL 1757
                        61 ATKOAEAAPVVESKWRAL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HCV NS4a; 1.
HCV NS4b; 1.
HCV NS5a; 1.
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Serum;
                                                                                                                                                                                                                                       NCBI_TaxID=11103;
                                                                                                                                                                                     Polyprotein.
                                                                                                                                                                                                                                                                                                                         Mishiro S.;
                                                                                                                                  Q9DTE4;
                                                                                                                    O9DTE4
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                                                                                                                                                                                                                                                                                                                                                          1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
                                                                                                                                                                                                                                                                                                     Gaps
Pfam; PF00271; Helicase C; 1.
Pfam; PF00298; Vizzl RdRP; 1.
SWART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Bredope protein; Glycoprotein; Nonstructural protein; PP01yprotein; Transmembrane SEQUENCE 3010 AA; 327325 MW; 3DE6CF249BD1151C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nagayama K., Kurosaki M., Enomoto N., Maekawa S.y., Miyasaka Y.,
Tazawa J.i., Izumi N., Marumo F., Sato C.;
"Time-related changes in full-length hepatitis C virus and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael S. 25:0016.

GO; GO:0019029; C:viral capsid; IEA.

GO; GO:0019029; C:viral capsid; IEA.

GO; GO:00019031; C:viral capsid; IEA.

GO; GO:00005524; F:ATP binding; IEA.

GO; GO:0000525; F:ATP-dependent helicase activity; IEA.

GO; GO:00003723; F:RNA-binding; IEA.

GO; GO:00003723; F:RNA-binding; IEA.

GO; GO:00005198; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:00005198; F:structural molecule activity; IEA.

GO; GO:0006508; P:proteclysis and peptidolysis; IEA.

GO; GO:0006508; P:pranscription; IEA.

GO; GO:0006509; P:viral genome replication; IEA.

GO; GO:0019087; P:viral transformation; IEA.
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                                                                                                                                                                                                                                             Length 3010;
                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                          Score 391; DB 2;
Pred. No. 8.5e-32;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO: 0019031; C:viral envelope; IE
GO; GO: 0008524; F:ATP binding; IEA.
GO; GO: 0008026; F:ATP binding; IEA.
GO; GO: 0003723; F:RNA binding; IEA.
GO; GO: 0008236; F:RNA-directed RNA p.
GO; GO: 0008236; F: serine-type peptic
GO; GO: 0008136; F: serine-type peptic
GO; GO: 0006138; F: serine-type and pe
GO; GO: 0006138; F: protecolysis and pe
GO; GO: 0006309; P: protecolysis and pe
GO; GO: 00019097; P: viral genome replic
InterPro; IPR000345; CytC. heme BS.
InterPro; IPR001410; DEAD.
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InterPro; IPR002521; HCV core.
InterPro; IPR002531; HCV env.
InterPro; IPR002531; HCV env.
InterPro; IPR000745; HCV NS4.
InterPro; IPR001490; HCV NS4b.
InterPro; IPR001490; HCV NS4b.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATKOAEAAAPVVESKWRAL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activity.";
Vizology 263:244-253(1999).
EMEL, AF165060; AAD56195.1; -.
PIR; PG0246; PG0246.
PIR; PG0246; PG0254.
PIR; PG0804; PG0554.
PIR; PG0804; PG0804.
PIR; PG0804; PG0804.
HSPP; QGJY29; PS0329.
HSPP; QGJY29; PS0329.
MSROPS; S29.002; Cintegral to
                                                                                                                                                                                                                                       99.2%;
                                                                                                                                                                                                                                                                      Local Similarity 98.7
nes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=11103;
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[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polyprotein.
NON_TER
NON_TER 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepacivirus.
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Q68K57;
                                                                                                                                                                                                                                                                                                                                           068K36
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Matches
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Q68K57
                                                                                                                                                                                                                                                                                         RESULT 13
Q68K36
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DR InterPro; IPR002166; HCV RdRP.

DR InterPro; IPR004109; Peptidase C.

DR InterPro; IPR004109; Peptidase C.

DR InterPro; IPR003003; Peptidase C.

DR InterPro; IPR003003; Peptidase C.

DR InterPro; IPR007095; RNA_DOI_DS_PS.

DR InterPro; IPR007094; RNA_DOI_DS_PS.

DR Pfam; PF01542; HCV_corp; 1.

DR Pfam; PF01542; HCV_corp; 1.

DR Pfam; PF01549; HCV_NS1; 1.

DR Pfam; PF01560; HCV_NS1; 1.

DR Pfam; PF01001; HCV_NS3; 1.

DR Pfam; PF01001; HCV_NS3; 1.

DR Pfam; PF01001; HCV_NS3; 1.

DR Pfam; PF01001; HCV_NS4; 1.

DR Pfam; PF01001; HCV_NS5a; 1.

DR Pfam; PF00271; Helīcase C; 1.

DR Pfam; PF00101; HCV_NS5a; 1.

DR Pfam; PF00271; Helīcase C; 1.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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MEDLINE=95146953; PubMed=7844535;
Greene W.K., Cheong M.K., Ng V., Yap K.W.;
"Prevalence of hepatitis C virus sequence variants in South-East
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97.5%; Pred. No. 4.2e-33;
ive 2; Mismatches 0; Indels
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J. Gen. Virol. 76:211-215(1995).
EMBL; U14254; AAC53943.1; ---
HSSP. P26663; ICUI.
GO; GO:0019012; C:virion; IEA.
InterPro; IPR00149; HCV NS4a.
InterPro; IPR001490; HCV NS4b.
Pfam; PF01001; HCV NS4a; 1.
Pfam; PF01001; HCV NS4b; 1.
Nonetructural protein.
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Best Local Similarity 97.5
Matches 77; Conservative
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nes 78; Conservative
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Q68218
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Kleiner D., Holman S., Augenbraun M., Taylor J.;
Kleiner D., Holman S., Augenbraun M., Taylor J.;
"Sequence Analysis of Hepatitis C Virus Replication Functions in TevroHIV Coinfected Subjects." i.
"HCV/HIV Coinfected Subjects." i.
"HCV/HIV Coinfected Subjects." i.
"HCV/HIV Coinfected Subjects." i.
"BMBL; AK685636; AAT94277.1; -.
"REMBL; AK685636; AAT94277.1; -.
"RINGEPPO; IPR001409; DEAD.
"RINGEPPO; IPR00145; DEAD/DEAH."
"InterPro; IPR00145; Peptidase C.
"InterPro; IPR001609; Peptidase S29.
"InterPro; IPR009003; Peptidase S29.
"InterPro; IPR009077; Helicase S29.
"InterPro; IPR009003; Peptidase S29.
"InterPro; IPR009003; Peptidase S29.
"InterPro; IPR009003; Peptidase S29.
"InterPro; IPR009003; Peptidase S29.
"InterPro; IPR009004; Peptidase S29.
"InterPro; IPR00904; Pept
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Hepacivirus:
NCBI_TaxID=11103;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Local Similarity 97.5%; Pred. No. 2.2e-32;
es 77; Conservative 2; Mismatches 0; Indels
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Hepatitis C virus.
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                   Gaps
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Hepacivirus.
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"Sequence Analysis of Hepatitis C Virus Replication Functions in "Sequence Analysis of Hepatitis C Virus Replication Functions in HCV/HIV Coinfected Subjects.";
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY685559; AAT9424.1;
InterPro; IPR01410; DEAD.
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Lamson D., Wroblewski D., Reilly A., Philpott S.,
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70593 MW; CFF7E6C7E0242545 CRC64;
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70411 MW; 2FCC6D44A67324E1 CRC64;
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99.0%; Score 390; DB 2;
Best Local Similarity 97.5%; Pred. No. 2.2e-32;
Matches 77; Conservative 2; Mismatches 0;
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Interpro; IPR001650; Helloase C.
Interpro; IPR004109; Peptidase S2
Interpro; IPR009003; Pept_Ser_Cys.
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Pfam; PF01006; HCV NS4s; 1.
Pfam; PF001006; HCV NS4s; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
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659 AA;
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99.0%; Score 390; DB 2; Length 659; 97.5%; Pred. No. 2.2e-32;

Query Match Best Local Similarity

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               1 SVVIVGRIILSGRPAVIPDREVLYQEFDEMEECASHLPYIEQGMQLAEQFKQKALGLLQT
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1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                            Run on:
                                                                                                                                                                                                               Title:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseqp1980s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003s:\* geneseqp2003bs:\* A\_Geneseq\_16Dec04:\* 1: geneseco1980... Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	no	Antigenic	HCV polyp	Hepatitis	Hepatitis	Hepatitis	HK12. 9/2	HCV NS4-N	HCV NS4-N		HCV NS4-N	HCV NS4-N	HCV NS4-N	Hepatitis	HCV NS4-N	Portion o	HCV NS4-N	Hepatitis								
	Description	Aab31698	Aar25865	Aaw41743	Ado36214	Ado79388	Aar25887	Aar29882	Aar29883	Aar29885	Aar29871	Aar29884	Aar29877	Aar80044	Aar29881	Aar12599	Aar29533	Aab36932	Aao18001	Aae15729	Aae15731	Aae15720	Aae15717	Aae15727	Aae15728	Aae15722
		,														•										
SOFIMERATES	ID	AAB31698	AAR25865	AAW41743	AD036214	AD079388	AAR25887	AAR29882	AAR29883	AAR29885	AAR29871	AAR29884	AAR29877	AAR80044	AAR29881	AAR12599	AAR29533	AAB36932	AA018001	AAE15729	AAE15731	AAE15720	AAE15717	AAE15727	AAE15728	AAE15722
	DB	4	~	7	æ	æ	7	~	7	7	~	7	7	7	7	~	7	4	Ŋ	Ŋ	'n	Ŋ	Ŋ	Ŋ	2	2
	Length DB	33	196	196	214	214	219	272	272	272	272	272	360	767	863	1250	1411	1736	1985	1985	1985	1985	1985	1985	1985	1985
de	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167
	Result No.		7	m	4	2	9	7	σ,	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aae15730 Hepatitis	Abu09574 HCV Met-N	Abu09575 HCV Met-N	Adj57846 HCV repli		Add67963 Hepatitis	Aaw01680 HCV NS2-N	Abg30601 Hepatitis	Abg30584 Hepatitis	Abg30591 Hepatitis	Abg30600 Hepatitis	Abg30581 Hepatitis	Abg30586 Hepatitis	Abg30593 Hepatitis	Abg30582 Hepatitis	Abg30580 Hepatitis	Abg30602 Hepatitis	Abg30587 Hepatitis	Abg30589 Hepatitis	Abg30599 Hepatitis	
AAE15730	ABU09574	ABU09575	ADJ57846	ADR38450	ADD67963	AAW01680	ABG30601	ABG30584	ABG30591	ABG30600	ABG30581	ABG30586	ABG30593	ABG30582	ABG30580	ABG30602	ABG30587	ABG30589	ABG30599.	
1985 5	1985 6	1985 6	1985 8	1985 8	2063 7	2201 2	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	2201 5	
100.0	100.0	100.0	100.0	100.0					100.0			_		100.0		100.0	100.0	100.0		1
167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	167	
26	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

### ALIGNMENTS

RESULT 1

AAB31698	8691
n	AAB31698 standard; peptide; 33 AA.
×	
AC	AAB31698;
ă	
Г	30-APR-2001 (first entry)
ă	
B	Antigenic epitope of the Hepatitis C Virus (HCV) NS4 protein.
×	
Σ	
<b>₹</b>	NS4a protein; HCV infection.
×	
So	Hepatitis C virus.
<b>3</b>	
Z S	WO200104149-A1.
<b>{</b>	1000 MAT OF
<u>.</u> }	18-JAN-2001.
ξ <u>μ</u>	07=:HH;-2000: 2000WO-US018704.
: ×	
H.	09-JUL-1999; 99WO-US015578.
×	
PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
×	
II.	Fields HA, Khudyakov YE;
ž i	
Z :	WPI; 2001-138316/14.
Ž	
E Ld	New (mosaic) polypeptides, useful as reagents in assays for the ure
PT	or monitoring of HCV intections and as components or anti-HCV vace.
F.	comprises antigenic groups of hepatitis C virus (HCV).
ğ	
PS	Claim 5; Page 39; 52pp; English.
×	
႘	
႘	virus (HCV) NS4 protein. The peptide comprises amino acids 1916-19
ပ္ပ	the HCV polyprotein. The specification describes antigenic epitope
ខ	NS4 protein and NS4a prote
ខ	antigenic peptides are useful as diagnostic reagents for detecting
ប្ដ	a biological sample. They are also useful for monitoring HCV infec
ပ္ပ	
ပ္ပ	comprising the peptides are useful for preventing, minimizing or re
႘	HCV infection in patients who have been exposed to HCV or to indivi
ပ္ပ	such as health care workers or blood product recipients, who are m
ខ្ល	scome exposed to HCV infection. The antigenic
႘	
ပ္ပ	proteins in a sample or for laboratory research purposes

The present sequence represents an antigenic epitope from a hepatitis C virus (HCV) NS4 protein. The peptide comprises amino acids 1916-1948 of the HCV polyprotein. The specification describes antigenic epitopes from HCV core protein, NS3 protein, NS4 protein and NS4a protein. The antigenic peptides are useful as diagnostic reagents for detecting HCV in a biological sample. They are also useful for monitoring HCV infection in a patient sample in addition to diagnosis. Pharmaceutical compositions comprising the peptides are useful for preventing, minimizing or reducing HCV infection in patients who have been exposed to HCV or to individuals, such as health care workers or blood product recipients, who are more likely to become exposed to HCV infection. The antigenic peptides are male also useful for generating antibodies which can be used to detect HCV proteins in a sample or for laboratory research purposes lagnosis Claim 5; Page 39; 52pp; English.

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New Hepatitis C virus (HCV) vaccine having a polynucleotide that encodes the polypeptide sequences of the HCV core and at least one other HCV protein, for use in medicine, particularly for manufacturing a medicament for treating HCV.
                                                                                                                                                                                                                                                             Protein contg. non-A non-B hepatitis antigen fragment - prepd. by culturing transformants transformed by vector contg. base sequence coding specified aminoacid sequences, used for detecting hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatotropic; virucide; vaccine; gene therapy; vaccine;
Hepatitis C virus; HCV; core protein; HCV infection; vaccination; NS4B.
                                                                                                                                                                                                                                                                                                                                                         The present sequence is a non-A non-B hepatitis virus (NANBH) or hepatitis C virus (HCV) antigen, useful for diagnosis or detection
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 167; DB 2;
100.0%; Pred. No. 9.8e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus (HCV) truncated NS4B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MARLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO36214 standard; protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 27; 78pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogilvie L;
                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 9; 53pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-NOV-2003; 2003WO-EP012793
                                                                                                                 91JP-00354708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-NOV-2002; 2002GB-00026722
                                                                                                                                               90JP-00412020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
tes 33; Conservative
                                                                                                                                                                              (SHIM/) SHIMOTONO K. (GREC ) GREEN CROSS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamblin PA,
                                                                                                                                                                                                                                WPI; 1993-260858/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-420613/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADO36225
               Hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004046175-A1
                                               JP05176774-A
                                                                                                                 18-DEC-1991;
                                                                                                                                               18-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004.
                                                                                20-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AD036214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brett S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus antigen expressed as recombinant in E.coli - useful for diagnosis of hepatitis C virus infection.
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-A non-B hepatitis virus; NANBH; hepatitis C virus; HCV; antigen; diagnosis; detection.
                                                                                                                                                                                                                                                                                                                                                                coli; diagnostic; reagent; type C hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 196;
                                              100.0%; Score 167; DB 4; Length 33; 100.0%; Pred. No. 1e-19; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 167; DB 2;
100.0%; Pred. No. 9.8e-19;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                     MRELIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW41743 standard; protein; 196 AA
                                                                                                                                                                                                                                  AAR25865 standard; protein; 196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 4; 66pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90JP-00304417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90JP-00304417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TOKU ) TOKUYAMA SODA KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-263663/32.
                                                                                                                                                                                                                                                                                                                                                                Recombinant vector;
                                                               Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                HCV polypeptide 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 196 AA;
                 Sequence 33 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 JP04179482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-NOV-11990;
                                                                                                                                                                                                                                                                                                 21-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-1992.
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                                                                                                                                                                                                                                                                AAR25865;
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                                                   Query Match
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Matches

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Gaps

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The invention describes a polynucleotide vaccine comprising a polynucleotide sequence (S1) encoding the Hepatitis C virus (HCV) Core protein and at least 1 other HCV protein, and causes expression of the proteins in cells (in which (S1) has been mutated or positioned relative to the polynucleotide sequence encoding the other HCV protein, so that to the polynucleotide sequence encoding the other HCV protein, so that the other HCV protein is reduced). Also described are: a method of preventing or treating an HCV infection in a mammal, comprising administering the vaccine cited above to a mammal; and a method of vaccine is cited above, coating the polynucleotide onco gold beads and delivering the gold beads into the Akin. HCV nucleic acids, polymeptides, host cells, vectors and into the Akin. HCV nucleic acids, polymeptides, host cells, vectors and cantibodies used in the mannfacture of a medicament for the treatment of vaccine is useful in the mannfacture of a medicament for the treatment of HCV. This is the amnino acid sequence of the truncated HCV NS4B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Hepatitis C virus (HCV) vaccine having a polynucleotide that encodes the polypeptide sequences of the HCV core, NS3, NS4B and NS5B proteins, for use in medicine, in particular for manufacturing a medicament for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HCV). The sequence is the translation sequence of a polynucleotide in which codon usage was altered to resemble that of highly expressed human genes. HCV vaccines of the invention comprise a polynucleotide that encodes the HCV proteins Core, NS3, NS4B and NS5B, and does not encode individual proteins. The proteins may be expressed as individual proteins or as fusion proteins. Preferred fusions include double fusions between NS4B and NS5B and NS5B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV; NS4A; vaccine; DNA immunisation; hepatotropic; virucide; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of the NS4A protein of hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 167; DB 8; Length 214; 100.0%; Pred. No. 1.1e-18; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 MNRLIAFASRGNHVSPTHYVPESDAARVTQIL 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogilvie L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus NS4B protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hamblin PA,
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N-PSDB; ADO79399.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004046176-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO79388;
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LID ADO79388

XXX ADO79388

XXX HCV,
XX 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR25876-95 are encoded by the claimed hepatitis C virus genes of the invention which have been inserted into an E. coli vector. These polypeptides are useful as diagnostic reagents for type C hepatitis and they may be produced efficiently by recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus antigen expressed as recombinant in E.coli - useful for diagnosis of hepatitis C virus infection.
vaccines are useful for the treatment or prevention of an HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Revised record issued on 09-SEP-2004 : Correction to feature table key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                           Gaps
                                                                                                                                                                                                                                                                                                        Recombinant vector; E. coli; diagnostic; reagent; type C hepatitis.
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                                                Length 214;
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                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 167; DB 2;
100.0%; Pred. No. 1.1e-18;
ive 0; Mismatches 0;
                                                100.0%; Score 167; DB 8;
100.0%; Pred. No. 1.1e-18;
iive 0; Mismatches 0;
                                                                                                                           158 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 190
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                                                                                                                                                                                                                                                                                                                                                                                                /note= "Sequence AAR25865"
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR29882 standard; protein; 272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 13; 66pp; Japanese.
                                                                                                                                                                                          AAR25887 standard; protein; 219 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90JP-00304417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90JP-00304417.
                                                                                                                                                                                                                                           (revised)
(first entry)
                                                  Query Match 100.
Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TOKU ) TOKUYAMA SODA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-263663/32.
N-PSDB; AAQ27014.
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                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 219 AA;
                           Sequence 214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          JP04179482-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                          09-SEP-2004
21-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         techniques
                                                                                                                                                                                                                   AAR25887;
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AAR29882
ID AAR2
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AAR29882;

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The sequences given in AAR29871-906 and AAR29533 are encoded by various clones of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the invention. These NS4-NS5 RAB sequencess were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the converted into cDNA using transcriptase in the presence of one of the pring primer pairs. The cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence analysis shows that these clones represent the core region and some upstream sequences of HCV. These polypeptides are thought to contain a highly hydrophilic region which can adopt a "turn structure" which is not an alpha helix or a beta sheet. These polypeptides are thought to act as antigen a beta sheet. These polypeptides are thought to act as antigen associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)
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                                                        Hepatitis C; Virus; HCV; serum; HC; allele; core; region; upstream; hydrophilic; beta sheet; antigen; determinant; antiserum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seki M, Honda Y, Takahashi K, Murakami T, Teranishi Y, Hayashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 167; DB 2; Length 272; 100.0%; Pred. No. 1.5e-18;
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                                                                                                                                                                                                                                                                                                                                           91JP-00172794.
91JP-00287008.
91JP-00332329.
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                                                                                 transcriptase, cDNA, primer,
turn structure, alpha helix,
                                                                                                                                                                                                                                                                                                                         91JP-00139268
                                                                                                                                                                                                                                                                                                                                                                                                            92JP-00099957
                                                            Clone; polypeptide; NS4-NS5;
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               HCV NS4-NS5 peptide N22-3.
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N-PSDB; AAQ32514.
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                                                                                                                                                  Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 272 AA;
                                                                                                                                                                                                                                                                                                                                           12-JUL-1991;
07-OCT-1991;
16-DEC-1991;
20-APR-1992;
                                                                                                                                                                                                                                                                              11-JUN-1992;
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26-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAR29871-906 and AAR29533 are encoded by various clones of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the include of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the patient solution. These NS4-NS5 RMA sequences were the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the converted into cDNA using transcriptase in the presence of one of the converted into cDNA using transcriptase in the presence of one of the converted into cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence analysis shows that these clones represent the core region and some upstream sequences of the CV. These polypeptides are thought to contain a highly hydrophilic region which can adopt a "turn structure" which is not an alpha helix or a beta sheet. These polypeptides are thought to act as antigen associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                      Clone, polypeptide, NS4-NS5, Hepatitis C, Virus, HCV; serum, HC; transcriptase, cDNA; primer, allele, core, region, upstream; hydrophilic; turn structure, alpha helix, beta sheet, antigen, determinant, antiserum.

    used for diagnosing

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hepatitis C virus gene and its encoded protein - and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 167; DB 2;
100.0%; Pred. No. 1.5e-18;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 224-25; 305pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honda Y, Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                   91JP-00139268.
91JP-00172794.
91JP-00287008.
91JP-00332329.
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                                                                                                                                                                                                                                                                                                                                                                                          92EP-00109812
                                                                                     (first entry)
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(first entry)
                                                                                                                              HCV NS4-NS5 peptide N22-1.
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nes 33; Conservative
                                                                 (revised)
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                                                                                                                                                                                                                                                          Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-1992;
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                                                            25-MAR-2003
26-APR-1993
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26-APR-1993
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16-DEC-1991
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Seki M,

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Gaps

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Indels

Query Match

Matches

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XXXX

His

Ala Thr

label= Thr,

Misc-difference

Misc-difference Misc-difference

label= Val,

Ser

label= Asn,

Misc-difference 46

Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference

'label= Glu,

Arg Lys

label= His, 'label= Arg,

Leu

label= Pro,

Misc-difference 153

Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference Misc-difference

Leu

label= Val,

'label= Ile,

label= His, label= Tyr,

Phe

label= Tyr, Gln,

label= Cys,

label= Ala,

label= Phe,

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The sequences given in AAR29871-906 and AAR29533 are encoded by various clones of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the interest of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the cinverted into the sequences were the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the converted into cDNA using transcriptase in the presence of one of the converted into cDNA sequences isolated represent different alleles of the same region of the HCV gene. Sequence analysis shows that these clones represent the core region and some upstream sequences of the converted and some upstream sequences of the the thought to contain a highly hydrophilic region which can adopt a "turn structure" which is not an alpha helix or a beta sheet. These polypeptides are thought to act as antigen a determinants and are highly reactive with antiserum raised against HCV-associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)
turn structure; alpha helix; beta sheet; antigen; determinant; antiserum
                                                                                                                                                                                                                                                                                                                                New hepatitis C virus gene and its encoded protein - used for diagnosing
                                                                                                                                                                                                                                                            Teranishi Y, Hayashi N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 272;
                                                                                                                                                                                                                                                                                                                                                 and vaccinating against hepatitis C virus infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 167; DB 2;
100.0%; Pred. No. 1.5e-18;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                            Murakami T,
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 229-31; 305pp; English.
                                                                                                                                                                                                                                                            Honda Y, Takahashi K,
                                                                                                                                                                                                                               (MITU ) MITSUBISHI KASEI CORP.
                                                                                                                                                        91JP-00172794.
                                                                                                                 92EP-00109812
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                                                                                                                                                                                     91JP-00332329
92JP-00099957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Lea 33; Conserve
                                                                                                                                                                                                                                                                                      WPI; 1992-417213/51.
N-PSDB; AAQ32516.
                             Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 272 AA;
                                                                                                                 11-JUN-1992;
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16-DEC-1991;
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                                                          BP518313-A2
                                                                                      16-DEC-1992
                                                                                                                                                                                                                                                             Seki M,
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The sequences given in AAR29871-906 and AAR29533 are encoded by various clones of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the invention. These NS4-NS5 RNA sequencess were isolated from the serum of a parient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32565-77. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different these clones represent the core region and some upstream sequences of HCV. These polypeptides are thought to contain a highly hydrophilic region which can adopt a frurn structure" which is not an alpha helix or region which can adopt a frurn structure" with a light of a beta sheet. These polypeptides are thought to act as antigen ceterminants and are highly reactive with antiserum raised against HCV-associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to
                                                                                                                                                             New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 193-94; 305pp; English.
WPI; 1992-417213/51.
                                                            N-PSDB; AAQ32502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone; polypeptide; NS4-NS5; Hepatitis C; Virus; HCV; serum; HC; transcriptase; cDNA; primer; allele; core; region; upstream; hydrophilic; turn structure; alpha helix; beta sheet; antigen; determinant; antiserum.
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HCV NS4-NS5 peptide N22-1, N22-3, H22-8, H22-9.

(revised)
(first entry)

25-MAR-2003 26-APR-1993

AAR29871;

Location/Qualifiers

Hepatitis C virus.

Key

Takahashi K, Murakami T, Teranishi Y, Hayashi N;

91JP-00172794. 91JP-00287008. 91JP-00332329. 92JP-00099957.

11-JUN-1991; 12-JUL-1991; 07-OCT-1991; 16-DEC-1991;

20-APR-1992;

92EP-00109812

11-JUN-1992; 16-DEC-1992.

EP518313-A2

91JP-00139268

(MITU ) MITSUBISHI KASEI CORP.

Honda Y,

Seki M,

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Gaps

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Indels

Conservative

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AAR29871 standard; protein; 272

RESULT 10

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/label= Thr, Met, Ala

label= Thr,

SXS

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Best Local Similarity 100.0%; Pred. No. 1.:
Matches 33; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                            transcriptase; cDNA; primer; allele; core; region; upstream; hydrophilic; turn structure; alpha helix; beta sheet; antigen; determinant; antiserum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murakami T, Teranishi Y, Hayashi N;
                                                                      Gaps
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                                                                      ö
                                               Length 272;
                                                                     Indels
                                           Query Match
100.0%; Score 167; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 33; Conservative 0; Mismatches 0;
                                                                                             1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                           MIRLIAFASRGNHVSPTHYVPESDAAARVTQIL 44
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                                                                                                                                                                              AAR29884 standard; protein; 272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki M, Honda Y, Takahashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                          91JP-00139268.
91JP-00172794.
91JP-00287008.
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                                                                                                                                                                                                                                                                                   Clone; polypeptide; NS4-NS5;
                                                                                                                                                                                                                                                                                                                                                                                                     92EP-00109812
                                                                                                                                                                                                                                                                                                                                                                                                                                                              91JP-00332329
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(first entry)
                                                                                                                                                                                                                                                             HCV NS4-NS5 peptide H22-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-417213/51.
 correct PN field.)
                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 272 AA;
                       Sequence 272 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1991;
                                                                                                                                                                                                                         25-MAR-2003
26-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-DEC-1991
                                                                                                                                                                                                   AAR29884;
                                                                                                                                                     RESULT 11
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Length 272;

100.0%; Score 167; DB 2;

Query Match

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The sequences given in AAR29871-906 and AAR29533 are encoded by various clones of the NS4-NS5 regions of the Hepatitis C Virus (HCV) gene of the invention. These NS4-NS5 RNA sequencess were isolated from the serum of a patient suffering from hepatitis C (HC). The isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer sequences given in AAQ32565-77. The sequences were then amplified using primer pairs. The cDNA sequences isolated represent different calleles of the same region of the HCV gene. Sequence analysis shows that these clones represent the core region and some upstream sequences of HCV. These polypeptides are thought to contain a highly hydrophilic region which can adopt a "turn structure" which is not an alpha helix or a beta sheet. These polypeptides are thought to act as antigen associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatitis C virus gene and its encoded protein - used for diagnosing vaccinating against hepatitis C virus infections.
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100.0%; Pred. No. 2.1e-18;
ative 0; Mismatches 0;
Pred. No. 1.5e-18;
Mismatches 0;
                                                                              33
                                                                                                               12 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murakami T,
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                                                                              1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL
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                                                                                                                                                                                                                                                                      AAR29877 standard; protein; 360 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takahashi K,
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91JP-00287008.
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Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV NS4-NS5 peptide 2217.
                                                                                                                                                                                                                                                                                                                                                                                   (revised)
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N-PSDB; AAQ32508.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 360 AA;
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07-OCT-1991;
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26-APR-1993
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89GB-00028562
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Best Local Similarity 100.
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non-B hepatitis virus.
                                                                                                                                                                         WPI; 1992-417213/51.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 863 AA;
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17-SEP-1991
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16-DEC-1991;
20-APR-1992;
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                                11-JUN-1992;
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          16-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                              AAT04565 encodes AAR80044 a hepatitis C virus (HCV) antigenic sequence. An antigen derived from the antigenic sequence was combined with a carrier protein (maltose binding protein) to produce a fusion protein, which can be used for the highly sensitive detection of HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                        Diagnosis of HCV infection - using a fused protein comprising a HCV
                                                                                                                                                   Maltose binding protein; MBP; non-A non-B; HCV; diagnosis; antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 767;
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100.0%; Pred. No. 5.6e-18;
ive 0; Mismatches 0;
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 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 44
                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 7-10; 10pp; Japanese.
                                                                                                                              Hepatitis C virus antigenic sequence.
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                                                          AAR80044 standard; protein; 767 AA
                                                                                                                                                                                                                                                                                                                                                                   antigen and a carrier protein.
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(first entry)
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Best Local Similarity 100...
Seat Local 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus.
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26-APR-1993
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                                                                                                       25-MAR-1996
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                                                                                AAR80044;
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                                   RESULT 13
                                               AAR80044
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The sequences given in AAR29871-906 and AAR29533 are encoded by various CC clones of the NS4-NS5 RNA sequencess were isolated from the serum of a invention. These NS4-NS5 RNA sequencess were isolated from the serum of a converted into cDNA using transcriptase in the presence of one of the primer pairs. The cDNA sequences isolated RNA sequences were converted into cDNA using transcriptase in the presence of one of the primer pairs. The cDNA sequences isolated represent different amplified calledes of the same region of the HCV gene. Sequence analysis shows that these clones represent the core region and some upstream sequences of CHCV. These polypeptides are thought to contain a highly hydrophilic cregion which can adopt a "turn structure" which is not an alpha helix or a beta sheet. These polypeptides are thought to act as antigen cdeterminants and are highly reactive with antiserum raised against HCV-associated antigens. See also AAQ32436. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New hepatitis C virus gene and its encoded protein - used for diagnosing and vaccinating against hepatitis C virus infections.
                                                                                                                                                                                                                                                                                                                                                              Hayashi N;
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100.0%; Pred. No. 6.5e-18;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 44
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                                                                                                                                                                                                                                                                                                                                                                  Murakami T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 212-16; 305pp; English
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                                                                                                                                                                                                                                                                                                                                                                  Seki M, Honda Y, Takahashi K,
                                                                                                      91JP-00172794.
91JP-00287008.
91JP-00332329.
92JP-00099957.
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92EP-00109812.
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The sequence was deduced from a non-structural (3') coding region sequence isolated from serum of humans infected by the PT-NANBH virus. The polypeptide is an antigenic portion of the virus and will be useful in the development of vaccines for inducing immunity in man to PT-NANBH. The invention covers PT-NANBH viral polypeptides having an amino acid asquence at least 90 per cent homologous with the sequence given here, or antigenic fragments of such homologous sequences. See also AAQ12236-40 and AAQ12242. (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                          Post-transfusional non-A non-B hepatitis poly:peptide(s) - and also DNA and antibodies used in diagnostic assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 167; DB 2; Length 1250; Best Local Similarity 100.0%; Pred. No. 1e-17; Matches 33; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                       Tedder RS, Barbara JAJ;
                                                                                                                                                                                                                                                                                          Claim 1; Page 88-97; 108pp; English.
90GB-00004414.
90GB-00004814.
                                                           (WELL ) WELLCOME FOUND LTD. (HIGH/) HIGHFIELD P.E.
                                                                                                                       Highfield PE, Rodgers BC,
                                                                                                                                                              WPI; 1991-187584/26.
N-PSDB; AAQ12241.
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27-FEB-1990;
03-MAR-1990;
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Search completed: August 12, 2005, 14:15:00 Job time : 35.6216 secs

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RESULT 1
US-08-324-977-48
                                                              August 12, 2005, 14:04:54; Search time 9.24324 Seconds (without alignments) 266.510 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/SB_COMB.pep:*
/cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-539-601-9
US-09-539-601-12
US-09-539-601-24
US-09-539-601-30
US-08-324-977-12
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                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-904-686A-48
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US-08-904-686A-1
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                                                                                                                                                                                    513545 seqs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
                                                                                                         US-09-758-308-4
167
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                                                                                                                       Perfect score:
                                                                                                                                                     Scoring table:
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                                                                                                                                 Sequence:
                                                                                                                                                                                       Searched:
                                                                  Run on:
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28         167         100.0         3010         2         US-08-384-616-14           29         167         100.0         3010         2         US-08-904-686A-14           31         167         100.0         3010         2         US-08-904-686A-14           31         167         100.0         3010         3         US-08-904-686A-14           32         167         100.0         3010         3         US-09-315-850-2           33         167         100.0         3010         3         US-09-315-850-14           34         167         100.0         3010         4         US-09-539-601-3           35         167         100.0         3010         4         US-09-539-601-3           36         167         100.0         3010         4         US-09-539-601-3           37         161         96.4         106         3         US-09-539-601-3           38         161         96.4         106         3         US-09-539-601-3           39         161         96.4         260         4         US-01-014-96-8           39         161         96.4         260         4         US-101-257-1 <tr< th=""><th>Sequence 66, App Sequence 75, App Sequence 89, App</th></tr<>	Sequence 66, App Sequence 75, App Sequence 89, App
0.0001 10000 0.0001 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.00000 0.00000 0.00000 0.00000 0.00000 0.000000	US-08-444-818-66 US-08-444-818-75 US-08-444-818-89
0.0001 10000 0.0001 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.0000 0.0000 0.00000 0.00000 0.00000 0.00000 0.00000 0.000000	
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228 167 229 167 229 167 229 167 239 23 24 167 24 24 161 161 161 244 161 161 161 161 161 161 161 161 161 1	96.4 4.4 4.4
22222222222222222222222222222222222222	161 161 161
	. 4 4 4 5 4 5

## ALIGNMENTS

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US-08-124-997-48

US-08-124-997-48

US-08-124-997-48

Patent No. 574739

APPLICANT: PURE, Isao

APPLICANT: PURE, Isao

APPLICANT: PURE, Isao

APPLICANT: PURE, Isao

APPLICANT: TARMIZANA, Akahisa

APPLICANT: TARMIZANA, Akahisa

APPLICANT: TARMIZANA, Akahisa

APPLICANT: TARMIZANA, Akahisa

APPLICANT: TORENITON: ODNA AND ANTIGEN POLYPEPTIDE

NUMBER OF SEQUENCES: 50

CORRESPONDENCES: 50

CORRESPONDENCES: 80

CORRESPONDENCES: 180

CORRESPONDENCES
```

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; Sequence 48, Application US/08904686A; Patent No. 5998130 GENERAL INFORMATION: GENERAL Hiroto
  TELEX: 440142
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
                                                                     : 151 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-904-686A-48
                                                                                                                                                                   US-08-384-616-48
                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: OKAYAWA, Hiroto
APPLICANT: FUKE, Isaco
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: DNA-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: DNA-AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amanetrong, Westerman, Hattori, McLeland &
ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Score 167; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 33; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC COMPATISH
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/769,996

FILING DATE: 02-0CT-1991

APPLICATION NUMBER: UP 2-167466

FILING DATE: 25-UNN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 2-30921

FILING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/635,451

FILING DATE: 09-NOV-1990

PRIOR APPLICATION NUMBER: US 07/635,451

FILING DATE: 28-DEC-1990

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1725 K St. N.W. Suite 1000 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stevens-Smith, Theresa M. REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/08384616
Patent No. 5847101
                                                                                                TELEX: 440142
INPORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
                                                                                                                                                              LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-324-977-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20006
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US-08-384-616-48
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APPLICANT: FURE. Isao
APPLICANT: FURE. Isao
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Namstrong, Westerman, Hattori, McLeland &
ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
          Length 151;
                                                                                                     Indels
Query Match 100.0%; Score 167; DB 2; Best Local Similarity 100.0%; Pred. No. 1.3e-18; Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
                                                                                                                                                                                                     1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                  54 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 86
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SOFTWARE:
SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
PRILING DATE:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
SOFTWARE:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
FILING DA
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FILING DATE: 28-DEC-1990
ATTONREY/AGENT INFORMATION:
NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERNCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INFORMATION:
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REGISTRATION NUMBER: 31,541
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100."
Matches 33; Conservative
                                                                                                                                                                                                                        MOLECULE TYPE: protein US-09-315-850-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Matches 33; Conserv
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US-09-539-601-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                             Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OXANAMA, Hiroto
APPLICANT: EUKE, Isao
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland &
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                           Query Match 100.0%; Score 167; DB 2; Best Local Similarity 100.0%; Pred. No. 1.3e-18; Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                 54 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-A01-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JC 2-167466
FILING DATE: 25-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JC 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UL-1993
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 30-UL-1993
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 30-UL-1993
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: US 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/635,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1725 K St. N.W. Suite 1000 CITY: Washington STATE: D.C. STATE: D.C. ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/635,451
FILING DATE: 28 DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLeland, Le-Nhung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/09315850; Patent No. 6217872; GENERAL INFORMATION:
                     INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
  (202) 659-2930
                                                                                                                            TOPOLOGY: linear;
; MOLECULE TYPE: protein US-08-904-686A-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Naughton
    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-315-850-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 167; DB 4; Length 1985; Pred. No. 3.3e-17;
                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/09539601C
Sequence 12, Application US/09539601C
SENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW
TILE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOCTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER PILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE PATENTIN Ver. 2.1
SOFTWARE PATENTIN Ver. 2.1
LENGTH: 1985
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                                                                                                                                                                                                                                                                                                                   0; Mismatches
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REFERENCE/DOCKET NUMBER: 9007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0957
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                      LENGTH: 151 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-09-539-601-12
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TAKAMIZAWA, Akahisa
YOSHIDA, Iwao
YOSHIDA, Iwao
YOSHIDO: NON-A, NON-B HEPATITIS VIRUS GENOMIC
VENTION: CDNA AND ANTIGEN POLYPEPTIDE
                                       TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENO TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland ADDRESSEE: A Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 167; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
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                                                                                                                                                                                                                                                                                                                    Diskette, 3.5 in, 1.44Mb
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
SOCTWAREN ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION NUMBER: UP 2-167466
FILING DATE: 25-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UL-1993
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: US 07/69,996
FILING DATE: 28-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/63,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INPROMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,231
REGISTRATION NUMBER: 36,231
REGISTRATION NUMBER: 36,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 900703D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application US/08384616; Patent No. 5847101; GENERAL INFORMATION:
APPLICANT: FUKE, Isao
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 440142
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                  20006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-08-384-616-12
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                                                                                                                                                                                                                                                  COUNTRY:
                            APPLICANT:
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         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1985;
                                                                                                                                                          RESULT 7
US-09-539-601-24
; Sequence 24, Application US/09539601C
; Patent No. 6630343
; GENERAL INFORMATION:
; APPLICANT: Bartenechlager, Ralf FW
; TILE OF INVENTION: Hepatitis C Virus Cell Culture System
; FILE REPERENCE: all sequences
; CURRENT FILING DATE: 1090-04-03
; CURRENT FILING DATE: 1999-04-03
; MUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C Virus Cell Culture System
FILE REFERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 1999-04-03
EARLIER FILING DATE: 1999-04-03
SOFTWARE: PATENTI VET: 2.1
SOFTWARE: PATENTI VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 167; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      891 MNRLIAFASRGNHVSPTHYVPESDAAARVTOIL 923
                                                                               1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                 1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
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    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-539-601-30
; Sequence 30, Application US/09539601C
; Patent No. 6630343
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Patent No. 5747339
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FURE, Isao
APPLICANT: MORI, Chisato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; CRGANISM: Hepatitis C virus US-09-539-601-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Hepatitis C virus US-09-539-601-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 33; Conservative
       33; Conservative
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US-08-324-977-12
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         Matches
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Gaps

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Indels

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Length 2013;

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Mismatches
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SOPTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
RIGH APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 31-AUG-1990
PRIOR APPLICATION NUMBER: JP 2-305605
FILING DATE: 30-JUN-1990
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUN-1991
PRIOR APPLICATION NUMBER: US 07/69,996
FILING DATE: 20-JUN-1993
PRIOR APPLICATION NUMBER: US 07/69,996
FILING DATE: 20-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/69,996
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLELANG LACENTON:
NAME: MCLELANG LACENTON:
TELEPAX: (202) 689-0357
TELEFAX: (202) 689-0357
TELEFAX: LENGTH: 2013 amino acids
ENGTH: AND ALICATION: AND ALICATION:
TELEPAX: (202) amino acids
ENGTH: 2013 amino acids
                                                                                                                                                                                                           Diskette, 3.5 in, 1.44Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-315-850-12
; Sequence 12, Application US/09315850
; Patent No. 6217872
; GENERAL INFORMATION:
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                                                                                                             ZIP: 20006
COMPUTER REDABLE FORM:
MEDIUM TYPE: Dist
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Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-904-686A-12
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APPLICANT: FUKE, Isao
APPLICANT: PUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: ARAMIZAMA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CONA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
                      NON-A, NON-B HEPATITIS VIRUS GENOMIC CDNA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                      TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMI
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 167; DB 2;
100.0%; Pred. No. 3.4e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                       ZURINIA CONTROLL TO THE TOTAL COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1916 MNRLIAFASRGNHVSPTHYVPESDAARVTQIL 1948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424

RIOR APPLICATION DATA:

APPLICATION NUMBER: 07/769,996

FILING DATE: 02-007-1991

APPLICATION NUMBER: JP 2-167466

FILING DATE: 25-0107-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-230921

FILING DATE: 31-A02-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-305605

FILING DATE: 09-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/635,451

FILING DATE: 28-DEC-1990

ATORNEY/AGENT INFORMATION:

NAME: Stevens-Smith, Theresa M.

REGISTRATION NUMBER: 36,007319
                                                                                                                                                         STREET: 1725 K St. N.W. Suite 1000 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEPAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 440142
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERIGICS:
LENGTH: 2013 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
  YOSHIDA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
US-08-904-686A-12
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APPLICANT:
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Gaps
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APPLICANT: FUKE, Isao
APPLICANT: MARI, Chisato
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: ONN-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000 STREET: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 167; DB 2; 100.0%; Pred. No. 3.4e-17;
                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0 SOPTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
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Gaps

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TITLE OF INVENTION: POLYMERASE AND TERMINAL NUCLEOTIDYL TRANSFERASE TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV) FILE REPERENCE: ITOOO2P CURENT APPLICATION NUMBER: US/08/952,981A CURRENT FILING DATE: 1998-03-23 NUMBER OF SEQ ID NOS: 14

SOFTWARE: PALENTIN VEY: 2.0

SEQ ID NO 2

LENGTH: 2201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09539601C; Sequence 6, Application US/09539601C; Patent No. 6630343; GENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW; TITLE OF INVENTION: Hepatitis C Virus Cell Culture System; TILE REFERENCE: all sequences; CURRENT APPLICATION NUMBER: US/09/539,601C; CURRENT FILING DATE: 2001-08-30; EARLIER PILING DATE: 1999-04-03; NUMBER OF SQL ID NOS: 51; SOFTWARE: Patentin Ver. 2.1; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 6; STANDER OF SQL ID NOS: 51; SQL ID NOS: 51; STANDER OF SQL ID NOS: 51; SQL ID NOS: 51; STANDER OF SQL ID NOS: 51
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GENERAL INFORMATION:
APPLICANT: Bartenschlager, Ralf FW
TITLE OF INVENTION: Hepatitis C virus Cell Culture System;
FILE REPERENCE: all sequences
CURRENT APPLICATION NUMBER: US/09/539,601C
CURRENT FILING DATE: 2001-08-30
EARLIER APPLICATION NUMBER: 199 15 178.4 GERMANY
EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 51
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 2201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 167; DB 3; Best Local Similarity 100.0%; Pred. No. 3.8e-17; Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 167; DB 4; Best Local Similarity 100.0%; Pred. No. 3.8e-17; Matches 33; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: CDNA clone pCD (38-9.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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; ORGANISM: Hepatitis C virus
US-09-539-601-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Hepatitis C virus US-09-539-601-6
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Best Local Similarity
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US-09-539-601-6
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US-08-952-981A-2
Sequence 2, Application US/08952981A
Patent No. 6383768
GENERAL INFORMATION:
APPLICANT: TOWEI. Licia
APPLICANT: BEHENS, Sven-Erik
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                 NUMBER OF SEQUENCES: 50
CORRESPONDENC ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 167; DB 3;
Best Local Similarity 100.0%; Pred. No. 3.4e-17;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
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APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-A0C-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 25-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2-230921
FILING DATE: 31-A0C-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/69,996
FILING DATE: 28-DEC-1991
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLELAND NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLELAND:
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
REGISTRATION NUMBER: 900703G
                                                                                                                   ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
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TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2013 amino acids
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Gaps

0; Gaps Matches 33; Conservative 0; Mismatches 0; Indels

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1 WNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33

ò q Search completed: August 12, 2005, 14:24:49 Job time : 10.2432 secs

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us-09-758-308-4.rup

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Hepacivirus.
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554.298 Million cell updates/sec
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                                                                                                          August 12, 2005, 14:03:18 ; Search time 30.4865 Seconds
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  1612378 segs, 512079187 residues
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POLG HCWBK
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Maximum Match 100%
Listing first 45 summaries
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2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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                 Copyright
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Query
Match 1
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    Q91AU0
Q99AU2
Q6GXR9
Q6GXR9
Q807P3
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Q81757
Q81760
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Q9DTD9
Q9DTD9
Q9DTE2
             167
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## ALIGNMENTS

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SEQUENCE FROM N.A. MEDLINE=97032798; PubMed=8878547; DOI=10.1006/bbrc.1996.1540; MEDLINE=97032798; PubMed=8878547; DOI=10.1006/bbrc.1996.1540; Yeh C.T., Chu C.M., Lidaw Y.F.; "Distinct composition of viral quasispecies between ascites and serum samples from patients with late stage chronic hepatitis C."; Blochem. Blophys. Res. Commun. 227:524-529(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98033184; PubMed=9367361;
MEDLINE=98033184; PubMed=9367361;
Yeh C.T., Lu S.C., Chu C.M., Liaw Y.F.;
"Molecular cloning of a defective hepatitis C virus genome from the ascitic fluid of a patient with hepatocellular carcinoma.";
J. Gen. Virol. 78:0-0(0).
                                                                                                                                                                                                                                                                                 Polyprotein.
Heparitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Last sequence update)
Last annotation update)
PRT; 1805 AA
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Pfam; PF01001; HCV NS4b; 1.
Pfam; PF01506; HCV NSSa; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF00998; Viral RGRP; 1.
                                                                                                            01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2004 (TrEMBLrel. 26,
     PRELIMINARY;
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Hepacivirus.
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R GO; GO:000525; 1DXP.

R GO; GO:000526; F:ATP binding; IEA.

GO; GO:000326; F:RATP dependent helicase activity; IEA.

GO; GO:000326; F:RNA binding; IEA.

GO; GO:000326; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:000326; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:000526; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:000520; P:RNA binding; IEA.

R GO; GO:0019087; P:Viral genome replication; IEA.

R GO; GO:0019087; P:Viral genome replication; IEA.

R GO; GO:0019087; P:Viral genome replication; IEA.

R InterPro; IPR00140; DEAD.

R InterPro; IPR00140; DEAD.

R InterPro; IPR00140; HVV NS4a.

InterPro; IPR00140; HVV NS4a.

InterPro; IPR001566; HCV NS4a.

InterPro; IPR001566; HCV NS4a.

InterPro; IPR001016; HCV NS3a.

InterPro; IPR001001; Peptidase S29.

R InterPro; IPR001001; Peptidase S29.

R InterPro; IPR001001; RNA_Pol_PSvir.

R Pfam; PF01001; HCV NS34; I.

R Pfam; PF01001; HCV NS34; I.
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                                                                                                                                                               Length 1805;
                                                                                            1805 AA; 195957 MW; 28D2FD07D0F5074B CRC64;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                        100.0%; Score 167; DB 2;
100.0%; Pred. No. 3.6e-15;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1984 AA
                                                                                                                                                                                                                          0; Mismatches
SMART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
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Best Local Similarity 100.
Matches 33; Conservative
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01-OCT-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
NS protein (Fragment).
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Best Local Similarity
Matches 33; Conserv
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                                                                  Polyprotein.
SEQUENCE 1
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SEQUENCE
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1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33

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MEDILINE=94333810; PubMed=8056334; DOI=10.1016/0378-1119(94)90008-6; Tanji Y., Hijikata M., Hirowatari Y., Shimotohno K.; "Identification of the domain required for trans-cleavage activity of hepatitis C viral serine proteinase."; Gene 145:215-219(1994).
                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein precursor.
Hepatitis C virus type 2.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95156583; PubMed=7853491;
Tanji Y., Hijikata M., Satoh S., Kaneko T., Shimotohno K.;
Tanji Y., Hijikata M., Satoh S., Kaneko T., Shimotohno K.;
Firepatitis C virus-encoded nonstructual protein NS4A has versatile
functions C virus protein processing.";
J. Virol. 69:1575-1881 (1395).
EMBL, D16435; BAA03905.1;
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Tanji Y., Hizikata M., Hirowatari Y., Shimotohono K.;
Tanji S., Hizikata M., Hirowatari Y., Shimotohono K.;
Thepatitis C virus polyprotein processing: kinetics and mutagenic
analysis of serine proteinase-dependent cleavage.";
J. Virol. 68:8418-8422(1994).
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GO; GO: 0019012; C: virion; IEA.

GO; GO: 0005524; F: ATP binding; IEA.

GO; GO: 00005524; F: ATP-dependent helicase activity; IEA.

GO; GO: 00003723; F: RNA binding; IEA.

GO; GO: 00003723; F: RNA binding; IEA.

GO; GO: 00003568; F: RNA-directed RNA polymerase activity; IEA.

GO; GO: 00005508; P: RNA-directed RNA polymerase activity; IEA.

GO; GO: 00005508; P: RNA-directed RNA polymerase; IEA.

GO; GO: 00005509; P: reanscription; IEA.

GO; GO: 0019087; P: viral genome replication; IEA.

GO; GO: 0019087; P: viral transformation; IEA.
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Hijikata M., Mizushima H., Tanji Y., Komada Y., Hirowatari Y.
Akagi T., Kimura K., Shimotohno K.;
"Proteolytic processing and membrane association of putative
nonstructural proteins of hepatitia C virus.";
Proc. Natl. Acad. Sci. U.S.A. 90:10773-10777(1993).
PRT; 2284 AA.
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IPRO09003; Pept Ser Cys.
IPRO02218; Pept U199 HCV NS2.
IPRO07095; RNA POL DS PS.
IPRO07094; RNA POL PSVIF.
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InterPro; IPR001410; DEAD.
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IPR001490; HCV NS4b.
IPR002868; HCV NS5a.
IPR002166; HCV RGRP.
                                                                                                                                                                                                        PRELIMINARY;
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PIR, P00246, P00246.
PIR, PS0329, PS0329.
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SEQUENCE FROM N.A.
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                                     InterPro;
InterPro;
InterPro;
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Hepacivirus.
NCBI_TaxID=11103;
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In virology 244:16-172(1998).

EMBL, 861962 A61196.

PIR, 861329, R620246.

PIR, P00246; P00246.

PIR, P00246; P00246.

R GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capeid; IEA.

GO; GO:0019028; C:viral envelope; IEA.

GO; GO:0019028; F:ATP-dependent helicase activity; IEA.

GO; GO:0003524; F:ATP-dependent helicase activity; IEA.

GO; GO:0003526; F:ATP-dependent helicase activity; IEA.

GO; GO:0003568; F:RAT-directed RNA polymerase activity; IEA.

GO; GO:0005269; F:RAT-directed RNA polymerase activity; IEA.

GO; GO:000529; F:Ratrocteolysis and peptidolysis; IEA.

GO; GO:0019079; P:viral genome replication; IEA.

GO; GO:0019079; P:viral transformation; IEA.

R GO; GO:0019079; P:viral transformation; IEA.

R GO; GO:0019079; P:viral transformation; IEA.

R GO; GO:00190740; P:viral transformation; IEA.

R GO; GO:00190740; P:viral transformation; IEA.

R InterPro; IPR0001410; DEAN.

R InterPro; IPR001410; DEAN.
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MEDLINE=98240944; PubMed=9581788; DOI=10.1006/viro.1998.9092;
Yanagi M., St Clare M., Shapiro M., Emerson S.U., Purcell R.H.,
Bukh J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 167; DB 2; Length 2284; 100.0%; Pred. No. 4.6e-15; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247213 MW; DC272A1517046337 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Pfam; PF0155.,
Pfam; PF02907; HCV_NS5; ...
Pfam; PF01006; HCV NS45; 1.
Pfam; PF01001; HCV NS45; 1.
Pfam; PF01506; HCV NS45; 1.
R Pfam; PF00291; Vival_RAF; 1.
R Pfam; PF00998; Vival_RAF; 1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
DR NONSTRUCTURAL DFOLEAL; POlyprotein; Signal.
FT SIGNAL SS 83 Potential.
FT SIGNAL SS 83 Potential.
FT SIGNAL 1093 NS5A.
NS5A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NS2.
Potential.
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NS4A.
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Best Local Similarity 100.0
Matches 33; Conservative
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SEQUENCE
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092973;
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092973
092973
AC 0929 AC 0929
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ENTITY OF A CHIMERIC Clone of hepatitis C virus genotype lb are infectious in vivo.";

RT 'Infectious in vivo.";

RI 'Infectious in vivo.";

RE Virology 244:161-172(19981-

REMBL; ARO15457; AAC15730.1; -.

REMBL; ARO1545; PAG196.

REMBL; RO0246; PQ0246.

REMBL; PQ0245; PQ0246.

REMBL; PQ0245; PQ0246.

REMBL; PQ0129; Cintegral to membrane; IEA.

RO; GO:0019028; Civiral capsid; IEA.

RO; GO:0019028; Civiral capsid; IEA.

RO; GO:0019028; Civiral capsid; IEA.

RO; GO:0019028; F:ATP binding; IEA.

RO; GO:0003028; F:RAP dependent helicase activity; IEA.

RO; GO:000368; F:RNA-directed RNA polymerase activity; IEA.

RO; GO:0008226; F:serine-type peptidase activity; IEA.

RO; GO:0008226; F:serine-type peptidase activity; IEA.
                                                                                                                                                                                                                                                                                                                                     Pfam; PF02907; HCV_NS3; 1.
Pfam; PF02907; HCV_NS3; 1.
Pfam; PF01006; HCV_NS4; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01098; Virāl_RdRP; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00487; DEXDC; 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
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Hepacivirus.
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MEDLINE=98240944; PubMed=9581788; DOI=10.1006/viro.1998.9092;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein (Fragment).
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InterPro; IPR001490; HCV NS4D.
InterPro; IPR002868; HCV NS5a.
InterPro; IPR002166; HCV RGRP.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR009003; Pept_Ser_Cys.
InterPro; IPR002518; Pept_J9 HCV NS2.
InterPro; IPR007095; RNA_Dol_DS_PS.
InterPro; IPR007095; RNA_Dol_DS_PS.
                                                                                                                                                                                                                                 Pfan, PP01543; HCV capsid; 1.
Pfam, PF01542; HCV core; 1.
Pfam; PF01539; HCV env; 1.
Pfam; PF01550; HCV NS1; 1.
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InterPro; IPR000745;
InterPro; IPR001490;
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InterPro; I
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Virology 244:1161-172(1998).
EMBL; AF054258; AAC15731.1; -.
PIR; P60246; P00246.
PIR; P60329; P80329.
HSSP; Q02828; 1NB4.
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Coat protein, Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.

NON TER 2864 2864
SEQUENCE 2864 AA; 310482 MW; 32CF23E5E59C4E59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
POlyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=HC-J4;
MEDLINE=98240944; PubMed=9581788; DOI=10.1006/viro.1998.9092;
Yanagi M., St Clare M., Shapiro M., Emerson S.U., Purcell R.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 167; DB 2; Length 2864; Best Local Similarity 100.0%; Pred. No. 5.9e-15; Matches 33; Conservative 0; Mismatches 0; Indels 0
      P:proteolysis and peptidolysis; IEA.
GO, GO:0006508; P:proteolysis and peptidolysis; IEAGO; GO:0006550; P:transcription; IEAGO; GO:0019079; P:viral genome replication; IEAGO; GO:0019079; P:viral genome replication; IEAGO; GO:0019087; P:viral transformation; IEAGO; GO:0019087; P:viral transformation; IEAGO; GO:0019087; P:viral transformation; IEAGO; GO:0019087; P:viral transformation; IEAGO; INTERPO; IPR00145; CytC_heme_BS.
INTERPO; IPR00145; DEAD/DEAH N.
INTERPO; IPR001519; HCV_Core.
INTERPO; IPR001519; HCV_NS4a.
INTERPO; IPR001490; HCV_NS4b.
INTERPO; IPR001490; HCV_NS4b.
INTERPO; IPR001490; PEPTIGASE S29.
INTERPO; IPR001490; PEPTIGASE S29.
INTERPO; IPR00109; RNA_POL_DS-PS.
INTERPOS HCV_END; I.
PERM: PF0153; HCV_END; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 2864 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1
                                                                                                                                                                                                                                                                                                            Pfam; PF01538; HCV_NS2; 1.
Pfam; PF02907; HCV NS3; 1.
Pfam; PF01006; HCV_NS4a; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01061; HCV_NSSa; 1.
Pfam; PF010998; Viral RdRP; 1.
SMART; SM00487; DEXDC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepacivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     092975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
092975
      셤
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"Transcripts of a chimeric clone of hepatitis C virus genotype 1b are
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PROSITE; SM00487, DESCRIPTIONE C; UNKNOWN 1.

Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.

NON TER 2864 2864

SEQÜENCE 2864 AA; 310416 MW; COCD3933ED07C6A5 CRC64:
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019031; C:viral envelope; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
GO; GO:0003968; F:RNA-directed RNA polymerase activity;
R GO; GO:0008236; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0008236; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0006369; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0006508; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0019079; P:viral genome replication; IEA.
R GO; GO:0019079; P:viral transformation; IEA.
R GO; GO:0019079; P:viral transformation; IEA.
R InterPro; IPR001410; DEAD.
R InterPro; IPR001545; DEAD/DEAH N.
InterPro; IPR002522; HCV_capsid.
R InterPro; IPR002521; HCV_capsid.
R InterPro; IPR002521; HCV_capsid.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 100.0%; Score 167; DB 2; Local Similarity 100.0%; Pred. No. 5.9e-15; nes 33; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; irrovato; ceres Gys. Interpro; IPR009003; Pept Ser Gys. Interpro; IPR002518; Pept U39 HCV NS2. Interpro; IPR007095; RNA pol DS PS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR002531; HCV_NS1.
IPR001745; HCV_NS4a.
IPR001490; HCV_NS4b.
IPR002868; HCV_NS5a.
IPR002166; HCV_NGRP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01543; HCV capsid; Pfam; PF01542; HCV capsid; 1. Pfam; PF01543; HCV cars; 1. Pfam; PF01569; HCV NS1; 1. Pfam; PF01569; HCV NS2; 1. Pfam; PF01001; HCV NS3; 1. Pfam; PF01001; HCV NS48; 1. Pfam; PF01001; HCV NS48; 1. Pfam; PF01506; HCV NS58; 1.
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"Transcripts of a chimeric clone of hepatitis C virus genotype 1b are
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PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
NON_TER 2864 2864
                                                                                                                                                                                                                                                                      Inflections in vivo."

Virology 244:161-172(1998).

R BMBL; AF054255; AAC15729.1; -.

R PIR; PQ0246; PQ0246.

R PIR; PQ0246; PQ0246.

R PIR; PQ0246; PQ0246.

R PIR; PQ02828; LNB4.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0009026; F:ATP binding; IEA.

GO; GO:0003026; F:ATP binding; IEA.

GO; GO:0003026; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:000326; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0006326; P:ranscription; IEA.

GO; GO:0004326; P:ranscription; IEA.

R GO; GO:0019087; P:viral genome replication; IEA.
                                                                                                                    MEDLINE=98240944; PubMed=9581788; DOI=10.1006/viro.1998.9092;
Yanagi M., St Clare M., Shapiro M., Emerson S.U., Purcell R.H.,
Bukh J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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InterPro; IPR002518; Pept U39 HCV NS2.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007094; RNA pol PSvir.
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InterPro; IPR011410; DEAD.
InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR002522; HCV capsid.
InterPro; IPR002521; HCV_core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001490; HCV_NS4b
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Pfam; PF01542; HCV core; 1.
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Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS5a; 1.
Pfam; PF00998; Viral_RGRP;
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                                                                   SEQUENCE FROM N.A.
MCBI_TaxID=11103;
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InterPro;
InterPro;
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InterPro;
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Q9WLK9
ID Q9WL)
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                      | Nicettoday 244:161-172(1998) | Nicettoday 244:161-172(1992) | Nicettoday 244:161-172(1992) | Nicettoday 245:190246 | Nicettoday 245:19024 | Nicettoday 245:190246 | Nicettoday 245
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2864 AA; 310481 MW; CGDEB415F4A1D1D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 100.0%; Score 167; DB 2; Local Similarity 100.0%; Pred. No. 5.9e-15; nes 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
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InterPro; IPR004109; PepTidase S29.
InterPro; IPR001003; Pept_US= Cys.
InterPro; IPR001095; RNA_Dol_DS_FS.
InterPro; IPR007094; RNA_Dol_DS_FS.
InterPro; IPR007094; RNA_Dol_DS_FS.
InterPro; IPR007094; RNA_Dol_DS_Vir.
Pfam; PP01543; HCV_caps.dl, 1.
Pfam; PP01543; HCV_caps.dl, 1.
Pfam; PP0159; HCV_NS1; 1.
Pfam; PP01001; HCV_NS3; 1.
Pfam; PP01001; HCV_NS4; 1.
Pfam; PP01001; HCV_NS4; 1.
Pfam; PP01001; HCV_NS4; 1.
Pfam; PP01001; HCV_NS4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR02522; HCV_capsid.
InterPro; IPR002519; HCV_core.
InterPro; IPR002519; HCV_env.
InterPro; IPR002519; HCV_NS1.
InterPro; IPR000745; HCV_NS4.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR001490; HCV_NS4b.
InterPro; IPR00166; HCV_NS4b.
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PROSITE; PS00190; CYTOCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepacivirus
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SEQUENCE
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Q9WLK8;
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Matches
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RESULT 8

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MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infectious in vivo.";
Virology 244:161-172(1998).
EMBL; AF054252; AAC15726.1; -.
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IPR001490; HCV_NS4b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002868; HCV_NS5a.
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Pfam; PF01001; HCV NS4b; 1
Pfam; PF01506; HCV NS5a; 1
                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A61196; A61196.
PIR; PQ0246; PQ0246.
PIR; PS0329; PS0329.
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Wirology 260804.
Wirology 260804.
Wirology 260804.
Wirology 260804.
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Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;
Polyprotein; Transmembrane.

NON_TER 2864
                                                                                                      Polyprotein (Fragment).
Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASSE, CONTROL C. SINTEGRAL TO MEMBLANE; IEA.

GO; GO: 0019028; C: viral capsid; IEA.

GO; GO: 0019028; C: viral capsid; IEA.

GO; GO: 0019021; C: viral capsid; IEA.

GO; GO: 0000524; F: ATP-binding; IEA.

GO; GO: 00003725; F: RATP-dependent helicase activity; IEA.

GO; GO: 0000325; F: RATP-dependent helicase activity; IEA.

GO; GO: 0000526; F: RETUCTURAL MOLECULE activity; IEA.

GO; GO: 0000526; P: proteolysis and peptidolysis; IEA.

GO; GO: 0019079; P: viral genome replication; IEA.

R GO; GO: 0019087; P: viral genome replication; IEA.

R INTERPRO: IPR000345; CytC heme BS.
                                                                                                                                                                                                                                                                                                                        MEDLINE=98240944; PubMed=9581788; DOI=10.1006/viro.1998.9092;
Yanagi M., St Clare M., Shapiro M., Emerson S.U., Purcell R.H.,
Bukh J.;
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                   01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 33; Conservative
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                                                                                                                                                                                                            NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                     Hepacivirus.
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"Transcripts of a chimeric clone of hepatitis C virus genotype 1b are
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-2004 (TrEMBLrel. 26, Last annotation update)
Polyprotein (Fragment).
Hepatitis C virus.
Niruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HESP: 002828; JUNE.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0019031; C:viral capaid; IEA.

R GO; GO:0019032; C:viral envelope; IEA.

R GO; GO:0008252; F:ATP binding; IEA.

R GO; GO:0008252; F:ATP dependent helicase activity; IEA.

R GO; GO:0003968; F:RNA binding; IEA.

R GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.

R GO; GO:0008256; F:serine-type peptidase activity; IEA.

R GO; GO:0008256; F:serine-type peptidase activity; IEA.

R GO; GO:0006508; P:protecolysis and peptidolysis; IEA.

R GO; GO:0006350; P:transcription; IEA.

R GO; GO:0019097; P:viral genome replication; IEA.

R GO; GO:0019097; P:viral transformation; IEA.

R InterPro; IPR000345; CytC heme BS.

R InterPro; IPR001410; DEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=HC-J4;
MEDLINE=9824094; PubMed=9581788; DOI=10.1006/viro.1998.9092;
MEDLINE=9824094; PubMed=9581788; DOI=10.1006/viro.1998.9092;
Yanagi M., St Clare M., Shapiro M., Emerson S.U., Purcell R.H.,
Bukh J.;
1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
                                                                                                                                                                                            PRT; 2864 AA.
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SMART; SM00487; DEXDĒ; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002166; HCV RdRP.
InterPro; IPR004109; Peptidase $29.
InterPro; IPR004109; Peptidase $29.
InterPro; IPR0051819; Pept_Srr_Cys.
InterPro; IPR007095; RNA_pol_DS_PS.
InterPro; IPR007095; RNA_pol_ES_FI.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01543; HCV_capsid; 1.
Pfam; PF01583; HCV_env; 1.
Pfam; PF01589; HCV_env; 1.
Pfam; PF01580; HCV_NS_1; 1.
Pfam; PF01581; HCV_NS_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IPR011545; DEAD/DEAH N. | IPR002522; HCV capsid. | IPR002521; HCV core. | IPR002519; HCV env. | IPR002531; HCV_NS1.
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RESULT 12
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EMBL; AR208024; AAF61205.1; -.

PIR; A61196; A61196.

PIR; P00246; PO0246.

PIR; PS0329; PS0329.

HSSP; QBJYS1; 1CWX.
                                                                                     Gaps
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
NON TER 2864 2864
SEQÜENCE 2864 AA; 310557 MW; 53464C5C744191D9 CRC64:
                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO: 0016021; C:integral to membrane; IEA.
R GO; GO: 0015028; C:viral capsid; IEA.
R GO; GO: 0013028; C:viral capsid; IEA.
R GO; GO: 0013031; C:viral envelope; IEA.
GO; GO: 0005231; F:ATP binding; IEA.
R GO; GO: 00003728; F:RNA binding; IEA.
R GO; GO: 00003728; F:RNA binding; IEA.
R GO; GO: 00003728; F:RNA binding; IEA.
R GO; GO: 00005286; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO: 00005286; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO: 00005286; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO: 00005286; F:RNA-directed RNA polymerase activity; IEA.
R GO; GO: 00190198; F:structural molecule activity; IEA.
R GO; GO: 0015079; P:viral genome replication; IEA.
R GO; GO: 019087; P:viral genome replication; IEA.
R InterPro; IPR000345; CytC. heme_BS.
                                                                                     ö
                                                               Length 2864;
                                                                                   Indels
                                                                                                                                                                                                    09J3F4;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                             Query Match
100.0%; Score 167; DB 2;
Best Local Similarity 100.0%; Pred. No. 5.9e-15;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                          1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
                                                                                                           1 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                         PRT; 3008 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR009003; Pept_Ser_Gys.
InterPro; IPR0012518; Pept_U39 HCV NS2.
InterPro; IPR007095; RNA_pol_DS_FS.
InterPro; IPR007094; RNA_pol_PSvir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR011545; DEAD/DEAH N.
InterPro; IPR002522; HCV_capsid.
InterPro; IPR002521; HCV_core.
InterPro; IPR002519; HCV_env.
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HCV RdRP.
Helicase (
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Pfam; PF01542; HCV_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01560; HCV NS1; 1.
PF01538; HCV NS2; 1.
PF02907; HCV NS3; 1.
                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Hepatitis C virus.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                              STRAIN=MD34;
                                                                                                                                                                                                                                                             Name=MD34;
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Q9J3F4
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 45, Last annotation update)
01-AUG-1992 (Rel. 45, Last annotation update)
02-OCT-2004 (Rel. 45, Last annotation update)
Genome polyprotein (Contains: Capsid protein C (Core protein B2
Genome polyprotein E1 (GP32) (GP35); Envelope glycoprotein B2
(GP68) (GP70) (NS1); Proteane P7; Nonstructural protein NS2 (PS0);
(EC 3.4.21.98); Nonstructural protein NS4A (P4); Nonstructural protein
NS4B (P27); Nonstructural protein NS5A (P56); Nonstructural protein
NS5B (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)].
Hepatitis C virus (isolate BK) (HCV).
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"Structure and organization of the hepatitis C virus genome isolated from human carriers.";
"J. Virol. 65:1105-1113(1991).
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MEDLINE=97015088; PubMed=8861916; DOI=10.1016/S0092-8674(00)81350-1;
Love R.A., Parge H.E., Wickersham J.A., Hostomsky Z., Habuka N.,
Moomawa E.W., Adachl T., Hostomska Z., Hostomsky Z., Habuka N.,
The crystal structure of hepatitis C virus NS3 proteinase reveals a trypsin-like fold and a structural zinc binding site.";
Cell 87:331-342(1996).
Pfam; PF01006; HCV NS4a; 1.
Pfam; PF01001; HCV NS4b; 1.
Pfam; PF01201; HCV NS5a; 1.
Pfam; PF00271; Helicase C; 1.
Pfam; PF00998; Viral_RGRP; 1.
SMART; SM00487; DEXDC; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS001190; PYTOCHROME C; UNKNOWN 1.
POlyprotein; Erreinsmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96335224; PubMed=8647104;
Borowski P., Heiland M., Oehlmann K., Becker B., Korneteky L.;
Non-structural protein 3 of hepatitis C virus inhibits
phosphorylation mediated by CAMP-dependent protein kinase.";
Eur. J. Biochem. 237:611-618(1996).
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                                                                                                                                                                                                                                                                                                             Length 3008;
                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                       3008 AA; 326835 MW; 99AE09E14C3109F4 CRC64;
                                                                                                                                                                                                                                                                                                             100.0%; Score 167; DB 2;
100.0%; Pred. No. 6.2e-15;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1914 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                1 MARLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 3010 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91140698; PubMed=1847440;
                                                                                                                                                                                                                                                                                                                                                100.08;
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1487-1500
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                                                                                                                                                                                                                                      Polyprotein;
SEQUENCE 3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepacivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HCVBK
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P26663;
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RNA-directed RNA polymerase (Potential).
Potential.
Charge relay system.
Charge relay system.
Charge relay system.
ATP (Potential).
DECH box.
                                                                             (Potential)
(Potential)
(Potential)
                                                                                                            (Potential)
(Potential)
(Potential)
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     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                      Callular aminopeptidase.
Capsid protein (Potential).
Matrix protein (Potential).
Major envelope protein E (Potential).
Nonstructural protein NS1/E2 (Potential).
Nonstructural protein NS2 (Potential).
Nonstructural protein NS3 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
                                         RNA! (W).
SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
SIMILARITY: Contains 1 peptidase 829 domain.
SIMILARITY: Contains 1 peptidase W19 domain.
precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in P1 and Ser or Ala in P1. CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate (RNA)(N).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-91192160; PubMed-1849488; DOI=10.1016/0014-5793(91)80322-T; X Acto N., Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso K., Obkoshi S., Shimotohno K.; Xato N., Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso K., Xato N., Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso K., Xato N., Hijikata M., Nakagawa M., Ootsuyama Y., Muraiso K., Xato N., Xato N., Xato M., Xato
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                                                                                                     Length 3010;
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100.0%; Score 167; DB 1;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 33; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                  1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
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MEROPS; S29.001; -.
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Capsid protein C (Potential).
Matrix protein (Potential).
Major envelope protein E (Potential).
Nonstructural protein NS1 (Potential).
Nonstructural protein NS2 (Potential).
Protease/helicase NS3 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
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                                                                                            INTERPEYO; JERUGOZ31; HCV_NS1.
INTERPEYO; JERUGOZ31; HCV_NS4a.
INTERPEYO; JERUGOZ868; HCV_NS5a.
INTERPEYO; JERUGOZ868; HCV_NS5a.
INTERPEYO; JERUGOZ868; HCV_NS5a.
INTERPEYO; JERUGOS03; PEPL_USFEYO.
INTERPEYO; JERUGOS03; PEPL_USFEYO.
INTERPEYO; JERUGOS03; PEPL_USFEYO.
INTERPEYO; JERUGONO3; PEPL_USFEYO.
INTERPEYO; JERUGONO3; PEPL_USFEYO.
INTERPEYO; JERUGONO3; RNA_DOI_DS_PS.
INTERPEYO; JERUGONO94; RNA_DOI_PSYIR.
PÉAM; PFO1543; HCV_COPE; 1.
PÉAM; PFO1543; HCV_COPE; 1.
PÉAM; PFO1559; HCV_NS1; 1.
PÉAM; PFO1559; HCV_NS1; 1.
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                         InterPro; IPR002521; HCV_core
InterPro; IPR002519; HCV env.
InterPro; IPR002531; HCV NS1.
InterPro; IPR000745; HCV_NS4a
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Removed from capsid protein C by the cellular aminopeptidase.
Capsid protein C (Potential).
Matrix protein (Potential).
Major envelope protein E (Potential).
Nonstructural protein NSI/E2 (Potential).
Nonstructural protein NS2 (Potential).
Nonstructural protein NS2 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
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ATP-binding; Coat protein; Core protein; Envelope protein;
Glycoprotein; Helicase; Hydrolase; Nonstructural protein; Polyprotein;
RNA-directed RNA polymerase; Serine protease; Transferase;
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Potential.
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Charge relay system (By similarity)
Charge relay system (By similarity)
DECH box.
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Pred. No. 6.3e-15;
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InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007094; RNA pol DS PSvir.
Pfam; PP01542; HCV capeid; 1.
Pfam; PP01533; HCV capeid; 1.
Pfam; PP01539; HCV can; 1.
Pfam; PP01539; HCV NS1; 1.
Pfam; PP01509; HCV NS2; 1.
Pfam; PP01006; HCV NS3; 1.
Pfam; PP01006; HCV NS4; 1.
Pfam; PP01001; HCV NS4; 1.
Pfam; PP01506; HCV NS5a; 1.
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01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92295714; PubMed=1318627; DOI=10.1016/0168-1702(92)90066-1;
Tanaka T., Kato N., Nakagawa M., Ootsuyama Y., Cho M.J., Nakazawa T.,
Hijikata M., Ishimura Y., Shimotohno K.;
"Molecular cloning of hepatitis C virus genome from a single Japanese carrier: sequence variation within the same individual and among carrier: sequence variation within the same individual and among carrier: sequence variation within the same individual and among the cred individuals.";

"Wicus Res. 23.953(1922).
-!- FUNCTION: The small proteins NS2A, NS2B, NS4A and NS4B are hydrophobic, suggesting a possible membrane-related function. NS3 and NS5 may play a role in the viral RNA replication.
-!- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral precursor polyprotein, commonly with Asp or Glu in the P6 position, Cys or Thr in Pl and Ser or Ala in Pl'.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + SUBUNIT: The virion of this virus is a nucleocapsid covered by a lipoprotein m and glycoprotein E. The nucleocapsid is a complex of protein c and mRNA.
-!- SIMILARITY: Contains 1 peptidase S29 domain.
-!- SIMILARITY: Contains 1 peptidase U39 domain.
                                                                                                                       000269;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
25-OCT-2004 (Rel. 45, Last amocation update)
Genome polyprotein [Contains: Capsid protein C (Core protein B Envelope glycoprotein E (GPS);
(GP69) (GP70) (NR1); Protein P7; Nonstructural protein NS2 (P21)
(EC 3.4.22...); Protease/helicase NS3 (P70) (Hepacivirin)
(EC 3.4.22...); Nonstructural protein NS4A (P4); Nonstructural protein NS5B (P60) (P70) (MNA-directed RNA POlymerase) (EC 2.7.7.48)].
                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                       1916 MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 1948
         MNRLIAFASRGNHVSPTHYVPESDAAARVTQIL 33
                                                                                                                 PRT; 3010 AA
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Pept_U39_HCV_N9PeptIdase_S29.
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HCV_core.
HCV_env.
HCV_NS1.
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                                                                                                               STANDARD;
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InterPro; IPR002522;
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InterPro; IPR002519;
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             Envelope giycoprotein El (GP32) (GP35); Envelope glycoprotein E2 (GP68) (GP70) (MS1); Protein P7; Nonetructural protein NS2 (P21) (EC 3.4.22.-); Protease/helicase NS3 (P70) (Hepacivirin) (EC 3.4.21.98); Nonstructural protein NS48 (P4); Nonstructural protein NS48 (P27); Nonstructural protein NS54 (P56); Nonstructural protein NS58 (P66) (P70) (RNA-directed RNA polymerase) (EC 2.7.7.48)]. Hepacitis C virus (isolate Taiwan) (HCV).
                                                                                                                                                                   Genome polyprotein [Contains: Capsid protein C (Core protein) (P22);
                                                                                                                                                                                                                                                                                                                                                         (RNA)(N).
SUBUNIT: The virion of this virus is a nucleocapsid covered by SUBUNIT: The virion of this virus is a nucleocapsid covered by lipoprotein envelope. The envelope consists of two proteins: protein M and glycoprotein E. The nucleocapsid is a complex of protein C and mRNA.
SIMILARITY: Contains 1 peptidase S29 domain.
SIMILARITY: Contains 1 peptidase U39 domain.
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| HCV_NSI.
| HCV_NSA.
| HCV_NSA.
| HCV_NSA.
| HCV_NSA.
| HCV_NSA.
| HCV_RGRP.
| HCV_RGRP.
| Pept_U3_HCV_NS2.
| Pept_U3_HCV_NS2.
| RNA_pol_DS_PS.
| RNA_pol_DS_PS.
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or send an email to license@isb-sib.ch).
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PIR; A40244; GNWVTW.
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HCV_core.
HCV_env.
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PDB; 1NS3; X-ray; C/D=1677-1690.
MEROPS; S29.001; -.
MEROPS; U39.001; -.
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Helicase C; 1.
Viral_RdRP; 1.
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InterPro; IPR009003;
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InterPro; IPR002522;
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                                                                                                                              Hepacivirus.
NCBI_TaxID=31645;
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Core protein (Potential).
Matrix protein (Potential).
Major envelope protein E (Potential).
Nonstructural protein NS1/E2 (Potential).
Nonstructural protein NS2 (Potential).
Protease/helicase NS3 (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
Nonstructural protein NS4A (Potential).
RNA-directed RNA polymerase (Potential).
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Charge relay system (By similarity)
Charge relay system (By similarity)
Charge relay system (By similarity)
DECH box.
3D-structure; ATP-binding; Coat protein; Core protein;
Envelope protein; Glycoprotein; Helicase; Hydrolase;
Nonstructural protein; Polyprotein; RNA-directed RNA polymerase;
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                                                    Query Match 100.0%; Score 167; DB 1; Length 3010; Best Local Similarity 100.0%; Pred. No. 6.3e-15; Matches 33; Conservative 0; Mismatches 0; Indels 0;
1189 1197
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1680 1688
3010 AA; 327047 MW; AAD267D55CDFE215 CRC64;
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Search completed: August 12, 2005, 14:21:21 Job time : 31.4865 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

August 12, 2005, 14:00:18; Search time 107.012 Seconds (without alignments) 368.645 Million cell updates/sec Run on:

US-09-758-308-5 Title:

554
1 KATCTTHHDSPDADLIBANL.....NPPLLESWKDPDYVPFVVHG 102 Perfect score: Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_16Dec04:\* geneseqp1980s:\* Database

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* geneseqp2004s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aab31699 Antigenic	Aar68622 HCV prote			Adf88597 Hepatitis	Aar62868 Korean-ty	Aar30616 Polypepti	Aar25118 Non-A, No	_	Aar53417 Blood tra	Aab36932 Hepatitis	Abu09574 HCV Met-N		Adr38450 Hepatitis	Aaw01680 HCV NS2-N	Aar20111 Non-A, no	Aar20091 Non-A, no	Aay06423 Non-A, no	Aar34580 Human hep		Aaw37129 Hepatitis		Adl17781 Hepatitis	Aar34468 Encoded b	Aae02357 Hepacivir
ΙD	AAB31699	AAR68622	AAR68864	AAR82694	ADF88597	AAR62868	AAR30616	AAR25118	AAR10743	AAR53417	AAB36932	ABU09574	ABU09575	ADR38450	AAW01680	AAR20111	AAR20091	AAY06423	AAR34580	ABB05639	AAW37129	AAR58590	ADL17781	AAR34468	AAE02357
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% Query Match Length DB	102	3010	3010	3010	3010	392	3010	299	228	3010	1736	1985	1985	1985	2201	3010	3010	3010	3010	447	449	483	483	3011	1038
* Query Match	100.0	100.0	100.0	100.0	100.0	94.0	94.0	93.9	93.5	93.1	92.8	92.8	95.8	92.8	92.8	95.8	92.8	92.8	92.4	92.2	92.2	92.2	92.2	92.2	92.1
Score	554	554	554	554	554	521	521	520	518	516	514	514	514	514	514	514	514	514	512	511	511	511	511	511	510
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		Aae15726 Hepatitis Aae15721 Hepatitis Aao18001 Hepatitis Aae15729 Hepatitis		Aae15728 Hopatitis Aae15722 Hepatitis Aae15730 Hopatitis Adj57846 HCV repli Add67963 Hepatitis
AAE02356 AAR10747 AAR10748	AAE15724 AAE15725 AAE15718 AAE15723	AAE15726 AAE15721 AAO18001 AAE15729	AAE15731 AAE15720 AAE15717 AAE15727	AAE15728 AAE15722 AAE15730 ADJ57846 ADD67963
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510 509 509	507 507 507	507 507 507	507 507 507 507	507 507 507 507
26 27 28	29 30 32	3 3 3 3 6 5 4 3	6 8 8 4 7 8 6 0	444 443 5443

## ALIGNMENTS

¥. AAB31699 standard; peptide; 102 (first entry) 30-APR-2001 AAB31699; RESULT 1 AAB31699 

Antigenic epitope of the Hepatitis C virus (HCV) NS5a protein.

Antigen; HCV; polyprotein; core protein; NS3 protein; NS4 protein; NS4 protein; HCV infection.

Hepatitis C virus.

WO200104149-A1.

18-JAN-2001.

07-JUL-2000; 2000WO-US018704.

99WO-US015578. 09-JUL-1999; (USSH ) US DEPT HEALTH & HUMAN SERVICES.

Khudyakov YE; Fields HA,

WPI; 2001-138316/14.

New (mosaic) polypeptides, useful as reagents in assays for the diagnosis or monitoring of HCV infections and as components of anti-HCV vaccines, comprises antigenic groups of hepatitis C virus (HCV).

Claim 6; Page 39; 52pp; English.

The present sequence represents an antigenic epitope from a hepatitis C virus (HCV) NS5a protein. The peptide comprises amino acids 2322-2423 of the HCV polyprotein. The specification describes antigenic epitopes from HCV core protein, NS3 protein, NS4 protein and NS4a protein. The antigenic peptides are useful as diagnostic reagents for detecting HCV in a biological sample. They are also useful for monitoring HCV infection in apatient sample in addition to diagnosis. Pharmaceutical compositions comprising the peptides are useful for preventing, minimizing or reducing HCV infection in patients who have been exposed to HCV or to individuals, such as health care workers or blood product recipients, who are more likely to become exposed to HCV infection. The antigenic peptides are also useful for generating antibodies which can be used to detect HCV proteins in a sample or for laboratory research purposes

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AAR68622

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Hepatitis C virus, HCV, non-A non-B, helicase gene; RNA helicase;
baculovirus, recombinant production.
213. .1215
label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation site
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label= N-linked glycosylation site
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/label= N-linked glycosylation site
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/label= N-linked glycosylation
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label= N-linked glycosylation
25. 327
label= N-linked glycosylation
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|Jabel= N-linked glycosylation
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/label= N-linked glycosylation
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label= N-linked glycosylation
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                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                 AAR68864 standard; protein; 3010
                                                                                                                                                              Hepatitis C virus RNA helicase.
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|abel= N |
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/label= N 5
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/label= N-
                                                                                                                                     (first entry)
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/label= N-
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/label= N-
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                                                                                                                                                                                                                              Hepatitis C virus.
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                 2272
                                                                                                            AAR68864;
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New HCV-originated proteinase active substance - used for site-specific cleavage by an intermolecular reaction and the purification thereof.
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                                                                        Gaps .
                                                                                                                1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                 1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
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                                              Length 102;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                    61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                  61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                  2419. .2420
/note= "Serine protease cleavage site"
                                                                                                                                                                                                                                                                                                                                                                 proteinase; serine; cleavage; hepatitis C virus; HCV
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                                                                                                                                                                                                                                                                                                                                        HCV protein cleavable with new serine proteinase.
                                            Score 554; DB 4;
Pred. No. 1.6e-56;
                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.6
Matches 102; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KAEN/) KAENNO K.
(SUMQ ) SUMITOMO METAL IND LTD.
(SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                                                                                                                                                                                                                AAR68622 standard; protein; 3010 AA
                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93JP-00105666
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                                                                                                                                                                                                                                                                                                                 (first entry)
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Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus; Virus.
                                                                                                                                                                                                                                                                                                     (revised)
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                       Sequence 102 AA;
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Cleavage-site
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16-OCT-1995
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Gaps

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Indels

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Length 3010;

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2212 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to the novel testing method for diagnosing liver cancer. The novel method comprises amplifying the amino terminal region of a hepatitis-C virus NS3 gene using a predetermined primer and determining the hepatitis-C virus in a base sequence of the obtained DNA fragment. The novel testing method is useful for diagnosing liver cancer and also used in a gene amplification technique, a clinical laboratory test reagent, a polymerase chain reaction, a base sequence analysis and genetic engineering. The method enables the detection of a hepatitis-C virus having high carcinogenicity with high specificity. This sequence represents the protein of the hepatitis-C virus NS3 gene of the
from the non-structral region. Partial proteinase sequences (AAR82692-93) are contained within this sequence. The proteinases can be used as anti-HCV agents. They can also be used to screen cpds. for their ability to inhibit their proteclytic activity. In this way proteinase inhibitors can be identified. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                        1 KATCTTHHDSPDADLIBANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diagnosing liver cancer, involves amplifying amino terminal region hepatitis-C virus gene using predetermined primer and determining hepatitis-C virus in base sequence of obtained DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver cancer; hepatitis-C virus; NS3 gene; carcinogenicity
                                                                                                                                                                                                                                                                          61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                             100.0%; Score 554; DB 2;
100.0%; Pred. No. 1.1e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus NS3 gene protein, SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                       ADF88597 standard; protein; 3010 AA
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                                                                                                                                                                                                                                                                                                                                 2212 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 2271
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                  The DNA used to then be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V proteinase active substance - which has activity as an anti-HCV and can be used to screen for proteinase inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a partial Hepatitis C Virus (HCV) polyprotein
                                                                                                                                                                                                                                                                                                           1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                              Gaps
                                                    hepatitis C virus helicase gene in baculovirus - useful for large ale prodn. of RNA helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hepatitis C virus, screening; inhibitor; proteolytic;
                                                                                                                                AAQ81559 encodes AAR68864 hepatitis C virus (HCV) RNA helicase. was used in the construction of an expression vector, which was transform a baculovirus host. The transformed baculovirus could used for the recombinant prodn. of HCV RNA helicase
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                                                                                                                                                                                                                                             Length 3010;
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/note= "partial proteinase; see AAR82692"
992. .1907
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/note= "partial proteinase; see AAR82693"
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                                                                                                                                                                                                                                                                                                                                                                          61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                              100.0%; Score 554; DB 2; 100.0%; Pred. No. 1.1e-54;
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial HCV non-structural polyprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KAEN/) KAENNO K.
(SUMQ ) SUMITOMO METAL IND LFD.
(SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR82694 standard; protein; 3010 AA
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                                                                                                      Claim 1; Fig 1-4; 9pp; Japanese
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92JP-00249240.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identification; cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus; Virus
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N-PSDB; AAT03960.
        1995-040330/06.
                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                 Sequence 3010 AA;
                        N-PSDB; AAQ81559
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                                                                     prodn.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-1992;
04-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                         2272
                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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No 6.

1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP

Gaps ö Length 3010; Indela 100.0%; Score 554; DB 7; 100.0%; Pred. No. 1.1e-54; ive 0; Mismatches 0;

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셤 8 셤 AAR62868

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2212 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPLRAEDDEGEISVP 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The polypeptide is that encoded by the full cDNA sequence of Korean hepatitis C virus (KHCV) cDNA, KHCV-LBC1. It or its fragments may be used in a specific and accurate method for detecting KRUV antibodies in the serum of hepatitis C patients. Antibodies directed against these polypeptides are useful for the purification of KCHV antigens and for the development of an improved diagnostic to detect KHCV antigens in a sample. The polypeptides may also be used in a vaccine for treatment and prevention of KHCV infection at a dosage of $-200 ug/peptide. (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA and polypeptide(s) from a new type of hepatitis C virus (KHCV) - for diagnosing and vaccinating against KHCV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen S29; NANBH; Hepatitis C; HCV; T064; T069; T06A; ELISA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 521; DB 2; Length 3010;
Pred. No. 7.5e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2272 AEILRKSRKFPPALPIWAPPDYNPPLLESWKDPDYVPPVVHG 2313
                                                                                              coded by Korean HCV full cDNA sequence LBC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                    So HS,
                                                                                                                                                                                                                                                                                                                                                                    Choi DY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-A, Non-B Hepatitis Virus antigen #9.
                                                                                                                                                                                                                                                                                                                                                                     Park YW, Lim KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR25118 standard; protein; 299
                                                                                                                              KHCV-LBC1; diagnosis; vaccine
                                                                                                                                                                                                                                                           92EP-00109753.
                                                                                                                                                                                                                                                                                       91KR-00009510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.0%;
94.1%;
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 94.1.
Best Local Similarity 94.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (revised)
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                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1993-001883/01.
N-PSDB; AAQ33282.
                                                                                                                                                                                                                                                                                                                                                                     Lee YB,
Yang JY;
                                                                                                                                                              Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3010 AA;
                                                                                                                                                                                                                                                                                                                                       (LUCK-) LUCKY
                                                                                                                                                                                                                                                                                          10-JUN-1991;
                                                                                                                                                                                                                                                           10-JUN-1992;
                               27-AUG-2003
25-MAR-2003
19-MAY-1993
                                                                                                                                                                                                                                                                                                         06-AUG-1991;
                                                                                              Polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
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                                                                                                                                                                                                                             07-JAN-1993
                                                                                                                                                                                             EP521318-A2
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   AAR30616;
                                                                                                                                                                                                                                                                                                                                                                       Cho JM,
Kim ST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                field.)
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2212 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The KHCV NS5-1.2 epitope is a preferred antigen for use in an immunodiagnostic kit for simultaneous detection of hepatitis C and B viruses. The kit comprises antigenic proteins from both viruses. The HCV protein is pref. one of KHCV CORE 14, KHCV 897, KHCV NS4F, KHCV NS4E1E2 or KHCV NS5-1.2 proteins; the HBV protein is pref. HBV CORE or Pre S2 SAg protein. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT -2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                        Korean-type hepatitis C virus; KHCV; non-A, non-B hepatitis; NANBH; viral non-structural protein; NS5-1.2; epitope; antigen; immunodiagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 one or
more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KATCTTHHDSPDADLIBANLLWRQEMGGNITRVESENKVVILDSPDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       Korean-type Hepatitis C Virus non-structural protein 5-1.2 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kit for simultaneous diagnosis of hepatitis B and C - comprising more hepatitis B and C virus antigenic proteins including one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                  2272 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 2313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 521; DB 2;
Pred. No. 6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; Virus (Korean-type)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR30616 standard; protein; 3010 AA.
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                                                                                                                                                                   AAR62868 standard; protein; 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-KR000039
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                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Choi DY, Kim
                                                                                                                                                                                                                              (revised)
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LUCK-) LUCKY CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-358478/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ73204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                          WO9425874-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitope(s).
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                                                                                                                                                                                                AAR62868;
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AAR30616 ID AAR3 XX

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93 XATCTTHHDSPDADLIEANLLWRQEWGGNITRVESENKVVILDSFDPLRAEEDEREVSVA 152
                                                                                                                                                                                                                                                                                                                         The DNA corresponding to an RNA isolated directly from infected human liver tissue or serum is used to synthesise CDNA. A library is constructed using a lambda gtil cloning system. This library is screened and cloned for antigenic activity. Clones isolated can be incorporated into a vector plasmid, which is then inserted into E.coli to give a transformant which expressed an antigenic protein having this amino acid sequence. The product may be used for the immunoassay of antibodies to NANBH antigen in samples of serum etc. for diagnostic purposes. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymerase chain reaction; PCR; amplify; primer; non-A, non-B hepatitis; NANBH; virus; blood transmissible; detection; hepatitis virus; RT-PCR; C100 antibody; HCV RNA; NS5 region.
                                                                                                                                                                                                                                                Antigenic protein specific for non-A, non-B hepatitis - and cDNA coding for it which corresponds to RNA of infected liver tissue or serum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 518; DB 2; Length 228;
Pred. No. 6.8e-52;
7; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 AEILRRTRREPPAIPVWARPDYNPPLIESWKDPDYVPPVVHG 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                      Σ
                                                                                                                                                                        Oshima
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                        Tsuchiya M,
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 4; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR53417 standard; protein; 3010
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             89JP-00192721.
89JP-00195413.
89JP-00205722.
89JP-0024528.
89JP-00245264.
89JP-00245268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 93.5%;
Local Similarity 90.2%;
hes 92; Conservative ?
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/label= Asp,
89JP-00189874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Leu,
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                                                                                                                                          SEIYAKU
                                                                                                                                                                      Arima T, Yamamoto O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Non-A.
non-B hepatitis virus.
                                                                                                                                                                                                     WPI; 1991-058149/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 228 AA;
                                                                                                                                                                                                                    N-PSDB; AAQ10524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Misc-difference
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                                                                                                                                     (CHUS ) CHUGAI
             27-JUL-1989;
29-JUL-1989;
03-AUG-1989;
10-AUG-1989;
21-SEP-1989;
19-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ10523-540
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is one of 12 claimed antigen sequences specific to NANBH virus. The antigens can be used singly or in combination in an ELISA diagnosis of hepatitis. See AAR24946 and AR25110-R251121. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-B hepatitis specific antigenic protein encoded by phage clone
                                                                                                                                                                                                                                                                                                                                                                 non-A non-B hepatitis virus antigen proteins - for highly specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-A non-B hepatitis; antigenic protein; NANBH; phage clone; immunoassay; antibodies; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEILRKPRRFPPALPIWARADYNPPLIEPWKDPDYVPPVVHG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.9%; Score 520; DB 2; 91.2%; Pred. No. 5.6e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                      Kazami J;
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 46-48; 80pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR10743 standard; protein; 228
                                                                                                                                                      90JP-00325434.
90JP-00325435.
91JP-00070231.
91JP-00179074.
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89JP-00184739
                                                                                                                          91WO-JP001662
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                                                                                                                                                                                                                                                                                     Sato A, Ida N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 91.2
1es 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   detection of hepatitis.
                Non-A.
non-B hepatitis virus.
                                                                                                                                                                                                                                                     IND INC.
                                                                                                                                                                                                                                                                                                                    WPI; 1992-217026/26.
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ25748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 299 AA;
                                                                                                                                                                                                                                                     TORA ) TORAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lambda HC2206
                                                                                                                                                                      29-NOV-1990;
16-JAN-1991;
19-APR-1991;
07-JUN-1991;
                                                             WO9209634-A1
                                                                                                                           29-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUL-1989;
19-JUL-1989;
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Gaps

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Blood-transmissible non-A non-B hepatitis virus DNA - used for detection

WPI; 1994-163130/20.

N-PSDB; AAQ63499

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(KAEN/) KAENNO K.

Claim 1; Page 8-20; 22pp; Japanese

of hepatitis virus

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label= Ser, Arg,
                                                      label= Gln, Pro,
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/label= Glu, Asp
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/label= Met, Ile
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92JP-00051885 92JP-00051885

10-MAR-1992; 10-MAR-1992;

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                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                         This sequence is encoded by the genome of a blood transmissible non-A, non-B hepatitis (NANBH) virus. The cDNA sequence was isolated using the primers given in AAQ63500-35. The amplified fragments are used in the detection of hepatitis virus. The target DNA was isolated from serum of chronically infected NANBH patients who were C100 antibody-positive and HCV RNA (NSS region) positive. Reverse transcription-PCR and PCR were performed on cDNA and the total human NANBH DNA was constructed from 23
                                                                                                                                                                                                                                                                                                                                                   KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                           Length 3010;
                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        2272 AEILRKSKKFPPALPIWARPDYNPPLLESWKSPDYVPPAVHG 2313
                                                                                                                                                                                                                                                                                                                                                                                                          AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus tTA gene fused to polyprotein region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NS3-5 polyprotein; virus activity; surrogate cell.
                                                                                                                                                                                                                                                                                             Score 516; DB 2;
Pred. No. 2.9e-50;
3; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BOEH ) BOEHRINGER INGELHEIM CANADA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB36932 standard; protein; 1736 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 63-68; 70pp; English.
                                                                                                                                                                                                                                                                                                93.1%;
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Best Local Similarity 92...
Best Match
You 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis C virus
                                                                                                                                                                                                                                                                      Sequence 3010 AA;
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27-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a nucleic acid encoding a Met-NS3-NS4A-NS4B-NS5A-NS5B (NS stands for non-structural protein from HCV) polypeptide appearing as ABU09574. The encoded polypeptide has sufficient protease
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/note= "Wild-type Gly-Asp-Asp substituted by Ala-Ala-Gly"
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                                                                                                                                                                                                                                                1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HCV; enzyme; non-structural protein; NS3; NS4A; NS4B; NS5A; NS5B;
adenoviral vector; HCV infection; vaccine; mutant; gene therapy;
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Colloca S;
                                                                                                                                                                                  Score 514; DB 4; Length 1736; Pred. No. 2.5e-50; 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-381708/36.
N-PSDB; ACA61111, ACA61112, ACA61113, ACA61118, ACA61119.
                                                                                                                                                                                                                                                                                                           (MERI ) MERCK & CO INC.
(RICE-) IST RICERCHE BIOL MOLECOLARB ANGELETTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HCV Met-NS3-NS4A-NS4B-NS5A-NS5B (inactivated).
                                                                                                                                                                                                                                                                                                                                                                                                                    ABU09574 standard; protein; 1985 AA.
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13-MAR-2002; 2002US-0363774P.
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Best Local Similarity 92.2'
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Cortese R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hepatitis C virus.
                                                                                                                                                        Sequence 1736 AA;
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activity to process itself to produce an NS5B protein that is carymatically inactive. Also included are a cultured recombinant cell comprising the novel nucleic acid, making an adenovector (comprising: comprising an adenovirus genome plasmid comprising a gene expression of cassette by homologous recombination between the novel nucleic acid and a nucleic acid comprising a first adenovirus region from base pair 1450 corresponding to either Ad5 or Ad6, a second adenovirus region from base pair 3511-5548 corresponding to Ad6, joined to the first region, a third adenovirus region from base pair 3549-28138 corresponding to Ad6, joined to the second region, a fourth adenovirus region from base pair 30818-33966 corresponding to Ad6, joined to the second region, a fourth adenovirus region from base pair 30818-33966 corresponding to Ad5 or from base pair 3089-33784 corresponding to Ad6, joined to the third region, and 40 rescond base pair 33967-35935 corresponding to Ad6, joined to the Court region, and 40 rescond from base pair 33967-35935 corresponding to Ad6 is in a fifth adenovirus region from base pair 33967-35935 corresponding to recombinant adenovirus plasmid), an adenovirus the from the tis produced by method above appearing as ACAG113 which has a humanised version of the polymore of the fivent and encodes the HCV inactivated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polyprotein, a recombinant nucleic acid comprising one or more Ad6 regions and a region not present in Ad6, where at least one Ad6 region is selected from BlA, BlB, B2A, B4, L1, L2, L4 and L5. The nucleic acid is useful as a component of an adenoviral vector or a DNA plasmid vaccine providing a broad range of antigens for generating an HCV-specific cell mediated immune response. The nucleic acid may also be used in treating patients infected with HCV. The present sequence is the HCV polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1247 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 514; DB 6;
Pred. No. 2.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MERI ) MERCK & CO INC.
(RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Mismatches
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Colloca 8
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13-MAR-2002; 2002US-0363774P.
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Best Local Similarity 91.2%;
Matches 93; Conservative
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Cortese R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1985 AA;
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Luzzago A,
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                                                                                                                               The invention relates to a nucleic acid encoding a Met-NS3-NS4A-NS5A (CC -NS5B (NS stands for non-structural protein from HCV) polypeptide appearing as AB109574. The encoded polypeptide has sufficient protease activity to process itself to produce an NS5B protein that is activity to process itself to produce an NS5B protein that is comprising the novel nucleic acid, making an adenovercen (comprising: (a) producing an adenovirus genome plasmid comprising a gene expression corresponding to either AG or AG, a second adenovirus region from base pair 1510 corresponding to AG, so income adenovirus region from base pair 3511-554 corresponding to AG, so accond adenovirus region from base pair 5542-2813 corresponding to AG, joined to the first region, a fourth adenovirus region from base pair 3514-554 corresponding to AG, joined to the second region, a fourth adenovirus region from base pair 3549-2813 corresponding to AG, joined to the second region, a fourth adenovirus region from base pair 3048-3396 corresponding to AG or from base pair 30789-33784 corresponding to AG, joined to the third region, and a fifth adenovirus region from base pair 3047-35935 corresponding to AG or from base pair 30789-33784 corresponding to AG, joined to the third region, base pair 30789-33784 corresponding to AG, joined to the third region, base pair 30789-33784 corresponding to AG, joined to the third region, base pair 30789-33784 corresponding to AG, joined to the third region, base pair 30789-33784 corresponding to AG, joined to the fourth region, and (b) rescuing the recombinant adenovirus plasmid), an adenovirus from the fourth region are appearing as AGA61113 which has a humanised version of the polyprotein, a recombinant mucleic acid comprising one or more AG polymucleotide of the invention and encodes the HCV inactivated providing a broad range of antigens for generating and AGA61113 which has a humanised version of the present sequence is the wild-type HCV patings infected with HCV. The present sequence is the wild-type HCV by and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1187 KATCTTHHVSPDADLIEANLLWRQEMGGNITRVESENKVVVLDSFDPLRAEEDEREVSVP 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                          New nucleic acid encoding a Met-N33-NS4A-NS4B-NS5A-NS5B polypeptide, useful as a component of an adenovector or DNA plasmid vaccine for preventing or treating hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus (isolate BK) NS3-NS5B polyprotein mutant Seg 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus; HCV; NS3; NS5A; non-structural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1247 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPVVHG 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 514; DB 6;
Pred, No. 2.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus replication activity; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADR38450 standard; protein; 1985 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                             Example 1; Fig 5; 231pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus (isolate BK)
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.8%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93; Conservative
   2003-381708/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1985 AA;
                 N-PSDB; ACA61114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-2004
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Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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   셤
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This invention relates to a novel method for producing a Hepatitis C virus (HCV) replicon having an increased replication activity.

Specifically, it refers to modifying an HCV replicon construct to encode an amino acid substitution in NS3 (a non-structural protein that along with NS4A, NS4B, NS5A and NS5B make up the virus replication machinery released in the form of a polyprotein). The present invention describes an amino acid substitution at a position corresponding to amino acid 232 of NS5A that confers improved cell culture replication activity compared to wild type HCV. The method is useful for facilitating the identification of broadly efficacious compounds against different HCV isolates and facilitating HCV research, where compounds that inhibit HCV replication have research and therapeutic applications in identifying overall efficacy and lack of the onset of HCV in a patient. This polypeptide sequence is the HCV NS3 HTD NSSB polyprotein based on HCV-BK with a 471M mutation (corresponds to a feature).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1187 KATCTTHHVSPDADLIEANLLWRQEMGGNITRVESENKVVVLDSFDPLRAEEDEREVSVV 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Making Hepatitis C virus (HCV) replicon having increased replication activity, useful in HCV research, comprises modifying HCV replicon construct to encode an amino acid substitution at a position corresponding to amino acid 470 of NS3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                             /note= "Wild type residue substituted for Ile, corresponds to posn 232 of NS5A" 1395. .1985 /note= "NS5B"
                                                      'note= "Wild type residue substituted for Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.8%; Score 514; DB 8; Length 1985; 91.2%; Pred. No. 2.9e-50; ive 5; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1247 AEILRKSKKFFPAAMPIWARPDYNPPLLESWKDPDYVPPVHG 1288
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                                                                               corresponds to posn 470 of NS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; SEQ ID NO 1; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Markel EJ;
                                                                                                                                                                                                                                 948. .1394
/note= "NS5A"
                                                                                                                                                                                                        note= "NS4B"
                                                                                                                                            /note= "NS4A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2004; 2004WO-US003726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2003; 2003US-0447318P.
note= "NS3"
                                                                                                                                                                    .947
                                                                                                                      .686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grobler J, Flores O,
                                                                                                                                                                             687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-635590/61.
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ses 93; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADR38452.
                                                                                                                                                                                                                                                                                              Misc-difference
                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004074507-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-2004.
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                                                                                                                      Protein
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                                                                                                                                                                                                                                                                                                                                                                                         Protein
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A novel method for reproducing in vitro the RNA-dependent RNA polymerase (RdRp) activity or the terminal nucleotidyl transferase (TNTase) activity cor encoded by hepatisis of virus (HCV), is characterised in that sequences contg. NS5B are used in the mixture. The method is used for assaying in vitro the activities of RdRp and TNTase encoded by HCV in order to contg. NS5B are used in the mixture. The method is used for assaying in certain the replaces, compounds that inhibit these enzymatic activities and therefore might interfere with the replication of the HCV. The present sequence comprises amino acids 810-3010 of the CV polyprotein and corresponds to NS2-NS5B proteins. CDNA encoding this protein was cloned between the NCOI and HindIII sites of pBlueBacIII to form pBac25. Another expression plasmid, pBac5B (containing cDNA encoding canno acids 2420-3010 of HCV; see AAWOIFO3) was also constructed.

Extracts of Bac25- or Bac5B-infected Sf9 cells contain a novel magnesium-dependent enzymatic activity that catalyses de novo RNA synthesis. This cativity was shown to be dependent on the presence of RNA, but independent of an added primer or of the origin of the input RNA condecule. As the products generated by extracts of Sf9 cells infected with either Bac35 or Bac5B-infected by extracts of Sf9 cells infected with either Bac35 or Bac5B-infected by extracts of Sf9 cells infected with either Bac35 or Bac5B-infected by extracts of Sf9 cells infected with either Bac35 or Bac5B-infected by extracts of Sf9 cells infected with either Bac35 or Bac5B-infected by extracts of Sf9 cells infected broadcated that the observed RdRp activity is encoded by the HCV NS5B corrector. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 17-OCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reproducing enzymatic activities of HCV in vitro - using sequences contg. NS5B for RNA-dependent RNA polymerase and terminal nucleotidyl
                                                                                                                                                                                                                                                                            Hepatitis C virus, HCV, non-structural protein, NS5B, polyprotein, RNA-dependent RNA polymerase, RdRp, terminal nucleotidyl transferase, TNTase, method, assay, in vitro activity, therapy, inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Behrens S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 26-34; 49pp; English.
                                           AAW01680 standard; protein; 2201 AA.
                                                                                                                                                                                                                                HCV NS2-NS5B non-structural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-IT000106.
                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus; strain BK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95IT-RM000343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               De Francesco R, Tomei L,
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transferase activities.
                                                                                                                                   (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-021225/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2201 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9637619-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAY-1995;
                                                                                                                                                            25-MAR-2003
19-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-1996.
                                                                                                                                      17-0CT-2003
                                                                                          AAW01680;
RESULT 15
                        AAW01680
                                                                                          8
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Search completed: August 12, 2005, 14:15:01 Job time : 108.012 secs

ö 1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60

1403 KATCTTHHVSPDADLIEANLLWRQEMGGNITRVESENKVVVLDSFDPLRAEEDEREVSVP 1462

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Sequence

Sequence 1 Sequence 4 Sequence 1 Sequence 6

US-08-444-818-40 PCT-US94-04174-17 US-07-853-985A-6

ALIGNMENTS

Sequence Seguence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 48, Application US/08537811
Sequence 48, Application US/08537811
Setent No. 5910405
GENERAL INFORMATION:
APPLICANT: CHO, JOONG MYUNG
APPLICANT: CHOI, DECG YOUNG
APPLICANT: SO, HONG SEOB
APPLICANT: SO, HONG SEOB
APPLICANT: KIM, CHUN HYUNG
APPLICANT: KIM, IN SOO
APPLICANT: KIM, JOO HO
TITLE OF INVENTION: IMPROVED HCV DIAGNOSTIC
TITLE OF INVENTION: AGENTS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE PENNIE L PAP
                US-09-539-601-15
US-09-539-601-3
US-09-539-601-21
US-09-539-601-21
US-09-539-601-27
US-09-539-601-37
US-09-539-601-39
US-09-539-601-39
US-08-539-601-39
US-08-539-601-39
US-08-710-637-1
US-08-710-637-1
PCT-US94-07280-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: DOS
SOFTHARE: F881SEQ Version 2.0
CURRENT APPLICATION NUMBER: US/08/537,811
PILING DATE: 24-0CT-1995
CLASSIFICATION NUMBER: PCT/KR94/00040
FILING DATE: 30-APR-1994
APPLICATION NUMBER: KR 93-7440
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: JOHGS, III, HALTY C
REGISTRATION NUMBER: 20.280
FERERROKC/DOCKET NUMBER: 8512-037-999
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ 1D NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1155 Avenue of the Americas CITY: New York
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266.510 Million cell updates/sec
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Sequence 36,
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1 KATCTTHHDSPDADLIEANL......NPPLLESWKDPDYVPFVVHG 102
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Sequence 5
Sequence 5
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Sequence 3
Sequence 3
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Sequence 1
Sequence 1
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Sequence 3
Sequence 3
                                                                                                                                                                               August 12, 2005, 14:04:54 ; Search time 28.57 Seconds
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 ~ 2005 Compugen Ltd.
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US-08-324-977-50

US-08-904-686A-50

US-08-922-981A-2

US-08-922-981A-2

US-08-924-616-32

US-08-904-686A-32

US-08-304-686A-32

US-08-315-850-32

US-08-315-850-32

US-08-315-850-36

US-08-314-616-36

US-08-314-616-36

US-08-314-616-2

US-08-314-616-2
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US-09-539-601-18
US-09-539-601-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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449
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                                                                                                                                                                                    Run on:
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440142
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TELEFAX: (2)
TELEX: 4401
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                                                                                                                                                                                                                      1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                      Gaps
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Patent No. 5747339

GENERAL INFORMATION:
APPLICANT: OCAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSE: Armstrong, Westerman, Hattori, McLeland & ADDRESSE: Armstrong, N.W. Suite 1000 CITY: Washington STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20006

COMPUTER: EDABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                           Length 392;
                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                    61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                             Query Match

94.0%; Score 521; DB 2;
Best Local Similarity 94.1%; Pred. No. 1.9e-55;
Matches 96; Conservative 2; Mismatches 4
                    FEATURE: OTHER INFORMATION: KHCV NS5-1.2, Fig. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GOTTWALES: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION NATA:
APPLICATION NUMBER: UP 2-167466
FILING DATE: 31-AUN-1990
PRIOR APPLICATION NUMBER: UP 2-230921
FILING DATE: 31-AUC-1990
PRIOR APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-AUL-1993
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 18-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/695,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
RECESTRATION NUMBER: 36,281
RECESTRATION NUMBER: 36,281
RECESTRATION NUMBER: 36,281
TELEFAN: (202) 887-0357
TELEFAX: (202) 887-0357
protein
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  MOLECULE TYPE:
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TELEX: 4'
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1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                     92.8%; Score 514; DB 1; Length 997; 91.2%; Pred. No. 4.9e-54; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PUKE, Isao
APPLICANT: PUKE, Isao
APPLICANT: PUKE, Isao
APPLICANT: PUKE, Chisaco
APPLICANT: TAMIZANA, Akahisa
APPLICANT: YOSHIDA, Iwao
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: CDNA, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA, AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 300
                                                                                                                                                                                                                                                                                                                                                    61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-0CT-1991
APPLICATION NUMBER: UP 2-167466
FILING DATE: 25-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: US 07/635,451
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stevens-Smith, Theresa M. REGISTRATION NUMBER: 36,281
REPERENCE/DOCKET NUMBER: 900703B
TELEPHONE: (202) 659-2930
TELEPHAX: (202) 687-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-384-616-50
; Sequence 50, Application US/08384616
; Patent No. 5847101
; GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 997 amino acid
                                                                                                                                                          Query Match
Best Local Similarity 91...
Best Similarity 91...
Conservative
                                                               TYPE: amino acid
TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-324-977-50
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1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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GENERAL INFORMATION:

APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: FUKA, Akahisa
APPLICANT: YOSHIDA, Iwao
ITILE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
ADDRESSEE: ATMATICAD, Westerman, Hattori, McLeland & ADDRESSEE: Armatrong, Westerman, Hattori, McLeland & ADDRESSEE: A maghton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                  Query Match
92.8%; Score 514; DB 2; Length 997;
Best Local Similarity 91.2%; Pred. No. 4.9e-54;
Matches 93; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-AUG-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 25-UN-1990
FILING DATE: 25-UN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PELLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
RELOR APPLICATION DATE:
APPLICATION NUMBER: JP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-ULI-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 50, Application US/09315850; Patent No. 6217872
               REFERENCE/DOCKET NUMBER: 9007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 897-0357
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 997 amino acids
31,541
                                                                                                                                                                  LENGTH: 997 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-904-686A-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-315-850-50
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                                                                                                                                                                                                    Length 997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: OKAYAWA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: AKANIZAMA
APPLICANT: TAKANIZAMA
APPLICANT: TAKANIZAMA
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: NON-B, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                               259 AEIIRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 300
                                                                                                                                                                                                                                                                                                                                                                                                  61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTY: U.S.A.

ZIP: 2006

ZIP: 2006

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/904,686A

FILING DATE: 01-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/324,977

FILING DATE: 18-OCT-1994

PRIOR APPLICATION NUMBER: UP 2-167466

FILING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 2-230921

FILING DATE: 31-AUG-1990

PRIOR APPLICATION NUMBER: JP 2-305605

FILING DATE: 09-NOV-1990

PRIOR APPLICATION NUMBER: JP 2-305605

FILING DATE: 09-NOV-1990

PRIOR APPLICATION NUMBER: JP 2-305605

FILING DATE: OP-NOV-1990

PRIOR APPLICATION NUMBER: JP 2-305605
                                                                                                                                                                                              92.8%; Score 514; DB 2;
91.2%; Pred. No. 4.9e-54;
tive 5; Mismatches 4;
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FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US 07/635,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/08904686A Patent No. 5998130 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLeland, Le-Nhung
                       SEQUENCE CHARACTERISTICS:
LENGTH: 997 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                              Query Match
Best Local Similarity 91.23
Matches 93; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                      ; MOLECULE TYPE: protein US-08-384-616-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
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OKAYAMA, Hiroto

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APPLICANT: DE FRANCESCO, Raffaele
APPLICANT: TOMEI, Licia
APPLICANT: TOMEI, Licia
APPLICANT: BEHRENS, Sven-Erik
TITLE OF INVENTION: METHOD FOR REPRODUCING IN VITRO THE RNA-DEPENDENT RNA
TITLE OF INVENTION: POLYMERASE AND TERMINAL NUCLEOTIDYL TRANSFERASE
TITLE OF INVENTION: ACTIVITIES ENCODED BY HEPATITIS C VIRUS (HCV)
FILE REFERENCE: ITO002P
CURRENT APPLICATION NUMBER: US/08/952,981A
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
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92.8%; Score 514; DB 3; Length 2201;
Best Local Similarity 91.2%; Pred. No. 1.4e-53;
Matches 93; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 92.8%; Score 514; DB 3; Length 997; Best Local Similarity 91.2%; Pred. No. 4.9e-54; Matches 93; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1463 AEILRKSKKFPRAMPIWARPDYNPPLLESWKDPDYVPFVVHG 1504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION DATE:
APPLICATION NAMES: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLELANG, LE-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMONICATION INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 997 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08952981A Patent No. 6383768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: cDNA clone pCD (38-9.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 2
LENGTH: 2201
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1823 KATCTTHHVSPDADLIEANLLWRQEMGGNITRVESENKVVVLDSFDPLRAEEDEREVSVP 1882
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APPLICANT: FUAL, Chisato
APPLICANT: MORI, Chisato
APPLICANT: YOSHIDA, INAO
APPLICANT: YOSHIDA, INAO
TITLE OF INVENTION: NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armetrong, Westerman, Hattori, McLeland &
ADDRESSEE: Armetrong, Westerman, Hattori, mcLeland &
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.8%; Score 514; DB 1; Length 2620; Best Local Similarity 91.2%; Pred. No. 1.8e-53; Matches 93; Conservative 5; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALPIE 2000
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/324,977
FILING DATE: 18-OCT-1994
PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 2-167466
FILING DATE: 25-JUN-1990
PRICR APPLICATION DATA:
APPLICATION NUMBER: JP 2-230921
FILING DATE: 31-AUG-1990
PRICR APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRICR APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
APPLICATION NUMBER: US 07/769,996
FILING DATE: 20-JUL-1993
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1991
APPLICATION NUMBER: 36,281
FILING DATE: 28-DEC-1990
ATTORNEY/AGGENT INFORMATION:
NAME: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 36,281
FILING DATE: 30-2071
FILING DATE: Stevens-Smith, Theresa M.
REGISTRATION NUMBER: 36,281
REFERENCE/DOCKET NUMBER: 36,281
FILING DATE: 1020 S69-2930
TTELEPAN: AADIA:
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TTELEPAN: TELEPAN: TELE
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INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2620 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1725 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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RESULT 8 US-08-384-616-32

Sequence 32, Application US/08324977; Patent No. 5747339; GENERAL INFORMATION:

US-08-324-977-32

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APPLICATE: YOSHIDA, IWAO
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYBEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MCLEIBAID LE NUMBER:
NAME: MCLEIBAID LE NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 900703G
TELECOMMUNICATION INPORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 867-0357
INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
                     Sequence 32, Application US/08904686A
                                                                                                                                             FUKE, Isao
MORI, Chisato
TAKAMIZAWA, Akahisa
                                                                                                                 OKAYAMA, Hiroto
                                                 Patent No. 5998130
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
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APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, ISAO
APPLICANT: WORI, Chisato
APPLICANT: MORI, Chisato
APPLICANT: YOSHIDA, Akahisa
APPLICANT: YOSHIDA, IWAO
ITILE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
ITILE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Narmstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
COUNTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
COMPUTER: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
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APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-007-1991
APPLICATION NUMBER: UP 2-167466
FILING DATE: 25-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M. REGISTATION NUMBER: 36-01990
ATTORNEY/AGENT INFORMATION:
NAME: Stevens-Smith, Theresa M. REGISTATION NUMBER: 36-01991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ 1D NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 2620 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.2'
Matches 93; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
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                                                                                                                                                                                                                                   1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
                                                                                                                                                                                    0; Gaps
                                                                                                                                  Query Match 92.8%; Score 514; DB 2; Length 2620; Best Local Similarity 91.2%; Pred. No. 1.8e-53; Matches 93; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                 61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPFVVHG 102
2620 amino acids
                                                                ; MOLECULE TYPE: protein US-08-904-686A-32
                        amino acid
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1883 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 1924

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RESULT 9 US-08-904-686A-32

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RESULT 11
US-08-324-977-36
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                   Sequence 32, Application US/09315850
; Sequence 32, Application US/09315850
; Patent No. 6217892
; GENERAL INFORMATION:
    APPLICANT: OKAYAMA, Hiroto
    APPLICANT: TOKAYAMA, Hiroto
    APPLICANT: TOKAYAMA, Akahisa
    APPLICANT: TAKANIZAWA, Akahisa
    APPLICANT: TAKANIZAWA, Akahisa
    APPLICANT: TOSHIDA, Iwao
    TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
    NUMBER OF SEQUENCES: 50
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Anstrong, Westerman, Hattori, McLeland & STREET: 1725 K St. N.W. Suite 1000
    STREET: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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92.8%; Score 514; DB 3; Length 2620;
Best Local Similarity 91.2%; Pred. No. 1.8e-53;
Matches 93; Conservative 5; Mismatches 4; Indels (
1883 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
ZIP: 20006
COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
SOFTWARE: ASTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASTEM: ASTEM: APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/04,686

FILING DATE: 01-AUG-1997

APPLICATION NUMBER: US 08/324,977

FILING DATE: 18-0CT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 2-167466

FILING DATE: 25-JUN-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: UP 2-230921

FILING DATE: 31-AUG-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/099,706

FILING DATE: 30-JUL-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/69,996

FILING DATE: 02-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/69,996

FILING DATE: 28-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: MCLEBRAN, LE-Nhung

RESISTRATION NUMBER: 91,541

FREISTRATION NUMBER: 91,541

FREISTRATION NUMBER: 900703G

TELECOMMUNICATION NUMBER: 91,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202) 659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2620 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein US-09-315-850-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                US-09-315-850-32
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1823 KATCTTHHVSPDADLIEANLLWRQEMGGNITRVESENKVVVLDSFDPLRAEEDEREVSVP 1882
1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
APPLICANT: FUKE, Isao
APPLICANT: TAKANIZAMA, Akahisa
APPLICANT: TAKANIZAMA, Akahisa
APPLICANT: TAKANIZAMA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONVIRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GURRENT APPLICATION DATA:

SOCTIMERA

SPELICATION NUMBER: US/08/224,977

FILING DATE: 18-OCT-1994

PRIOR APPLICATION NUMBER: UP 2-167466

FILING DATE: 25-UN-1990

PRIOR APPLICATION NUMBER: UP 2-230921

FILING DATE: 31-AUG-1990

PRIOR APPLICATION NUMBER: UP 2-305605

FILING DATE: 30-UN-1990

PRIOR APPLICATION NUMBER: US 08/099,706

FILING DATE: 30-UL-1993

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/099,706

FILING DATE: 30-UL-1993

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/69,996

FILING DATE: 28-DEC-1991

PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/635,451

PRIOR APPLICATION NUMBER: US 07/635,451

REGISTRATION NUMBER: 36,281

REGISTRATION NUMBER: 36,281

REGISTRATION NUMBER: 36,281

REGISTRATION NUMBER: 36,281

TELLEPAN: (202) 659-2930

TELLEPAN: (202) 687-0357
                                                                                                                                                                                                                                                                                        Sequence 36, Application US/08324977
Patent No. 5747339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 440142
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2621 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-324-977-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FUKE, ISAO
APPLICANT: WORI, Chisato
APPLICANT: MARMIZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: TAKAMIZAMA, Akahisa
APPLICANT: YOSHIDA, IWAO
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF SEQUENCES: 50
CORRESPONDENCE ALOBRES:
ADDRESSEE: Armstrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
CITY: Washington
STATE: D.C.
Query Match 92.8%; Score 514; DB 2; Length 2621; Best Local Similarity 91.2%; Pred. No. 1.8e-53; Matches 93; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                     ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686A
FILING DATE: 01-AUG-1997
FILING DATE: 01-AUG-1997
FILING DATE: 18-CCT-1994
FILING DATE: 18-CCT-1994
FILING DATE: 18-CCT-1994
FILING DATE: 18-CCT-1994
FILING DATE: 25-JUN-1990
FILING DATE: 30-AUM-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2-230921
FILING DATE: 09-NOV-1990
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-AUL-1993
FRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 30-AUL-1993
FRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 30-AUL-1993
FRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 20-CCT-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DCCT-1991
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DCCT-1991
APPLICATION NUMBER: US 07/635,451
FILING DATE: 28-DCCT-1990
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/635,451
FILING DATE: 28-DCCT-1990
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/635,451
FILING DATE: ABDATE: US 07/635,451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               900703G
                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/08904686A
Patent No. 5998130
GENERAL INFORMATION:
APPLICANT: OKAYAMA, Hiroto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McLeland, Le-Nhung
REGISTRATTON UNDRER: 31,541
REBERENCE, DOCKET NUMBER: 9007
TELECOMMUNICATION INFORMATION:
TELEFAM: (202) 887-0357
INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
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COUNTRY: U.
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US-08-904-686A-36
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                                                                                                                        1823 KATCTTHHVSPDADLIEANLLWRQEMGGNITRVESENKVVVLDSFDPLRAEEDEREVSVP 1882
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                                                                                               1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                 US-08-384-616-36
Sequence 36, Application US/08384616
Sequence 36, Application US/08384616
GENERAL INFORMATION:
APPLICANT: OKAYAWA, Hiroto
APPLICANT: FUKE, ISAO
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: OF INVENTION: ONN-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: ONN-A, NON-B HEPATITIS VIRUS
TITLE OF INVENTION: ONN-A, NON-B HEPATITIS SEQUENCES: 50
CORRESPONDENCE ADDRESS:
  Score 514; DB 1; Length 2621;
Pred. No. 1.8e-53;
5; Mismatches 4; Indels (
                                                                                                                                                                                                                       ADDRESSEE: Armetrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton STREET: 1725 K St. N.W. Suite 1000 CITY: Washington
                                                                                                                                                                                            61 AEILEKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 900703B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEPAX: (202) 887-0357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 440142
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
       Query Match 92.8%;
Best Local Similarity 91.2%;
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2621 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
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APPLICANT: OKAYAMA, Hiroto
APPLICANT: PUKE, Isac
APPLICANT: TOKE, Isac
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TAKAMIZAWA, Akahisa
APPLICANT: TOSHIDA, Iwao
TITLE OF INVENTION: CDNA, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA, AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amanetrong, Westerman, Hattori, McLeland &
ADDRESSEE: Naughton
                                                                                                                                                                                                                                                                                                         92.8%; Score 514; DB 3; Length 2621; 91.2%; Pred. No. 1.8e-53;
                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1883 AEILRKSKKFPAAMPIWARPDYNPPLLESWKDPDYVPPVVHG 1924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFTWARE: ASCII
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/324,977
PILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-167466
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION NUMBER: US 09/099,706
FILING DATE: 09-NOV-1990
PRIOR APPLICATION NUMBER: US 08/099,706
FILING DATE: 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1990
APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08324977
Patent No. 5747339
REFERENCE/DOCKET NUMBER: 9007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEPAX: (202) 887-0357
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 2621 amino acids
                                                                                                                                                                                                                                                                                                                                                                93; Conservative
                                                                                                                                                                                     TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-315-850-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-324-977-2
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                                                                                                                                                                                                                                       1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                          Gaps
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                                                                                                                                Query Match
92.8%; Score 514; DB 2; Length 2621;
Best Local Similarity 91.2%; Pred. No. 1.8e-53;
Matches 93; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OCKAYAWA, HIROLO
APPLICANT: FUKE, Isao
APPLICANT: FUKE, Isao
APPLICANT: MORI, Chisato
APPLICANT: TARMIZAMA, Akahisa
APPLICANT: YOSHIDA, Iwao
TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOMIC
TITLE OF INVENTION: CDNA AND ANTIGEN POLYPEPTIDE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Armetrong, Westerman, Hattori, McLeland & ADDRESSEE: Naughton
STREET: 1725 K St. N.W. Suite 1000
                                                                                                                                                                                                                                                                                                                                           61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
SOFFWARE: ASCII
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/315,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICK APPLICATION DATA:
APPLICATION NUMBER: US/08/904,686
FILING DATE: 01-A01-1997
APPLICATION NUMBER: US 08/324,977
FILING DATE: 18-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/324,977
FILING DATE: 25-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JS 2-230921
FILING DATE: 31-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JS 2-305605
FILING DATE: 09-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,706
FILING DATE: 30-JUL-1993
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 02-OCT-1991
PRIOR APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
ATTORNEY APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
ATTORNEY APPLICATION NUMBER: US 07/769,996
FILING DATE: 28-DEC-1991
ATTORNEY APPLICATION NUMBER: US 07/763,451
FILING DATE: 28-DEC-1991
ATTORNEY APPLICATION NUMBER: US 07/763,451
FILING DATE: 28-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-315-850-36
; Sequence 36, Application US/09315850
; Patent No. 6217872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Le-Nhung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: McLeland, Le-N
REGISTRATION NUMBER:
                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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US-08-904-686A-36
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us-09-758-308-5.rpr

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 12, 2005, 14:04:14; Search time 20.2998 Seconds (without alignments) 483.460 Million cell updates/sec

US-09-758-308-5 554 1 KATCTTHHDSPDADLIEANL......NPPLLESWKDPDYVPPVVHG 102 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

beta-fructofuranos	nodulin precursor	probable pheT prot	enterochelin ester	nitrate reductase	hydrogenase (EC 1.	probable glycerald	hypothetical prote	hypothetical prote	chemotaxis protein	intermediate filam	hypothetical prote	probable transcrip	hypothetical prote	probable iles prot	probable oxidoredu
T06163	S08343	E70620	BVECES	G72603	C70358	C69466	A95870	D71101	T46614	S26432	F86244	T37518	S01956	E70760	F85774
7	~	7	~	0	~	N	N	~	0	N	N	N	~	~	~
584	309	831	374	466	633	340	398	450	753	432	554	603	1844	1041	239
12.5	12.5	12.5	12.4	12.4	12.4	12.2	12.2	12.2	12.2	12.1	12.1	12.1	12.1	12.0	11.9
69.5	69	69	68.5	68.5	68.5	67.5	67.5	67.5	67.5	67	63	67	67	66.5	99
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1
GNWVCJ
genome polyprotein - hepatitis C virus (strain J)
N; Contains: capsid protein C; envelope protein M; major envelope protein E; nonstructur
protein NS4a, nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 09-Jul-2004
20000C CL000C

R.Kato, N.; Hijikata, M.; Ootsuyama, Y.; Nakagawa, M.; Ohkoshi, S.; Sugimura, T.; Shimo Proc. Natl. Acad. Sci. U.S.A. 87, 9524-9528, 1990.
A.T.Tele: Molecular cloning of the human hapatitis C virus genome from Japanese patients A;Reference number: A39253; MUID:91088550; PMID:2175903

A;Molecule type: genomic RNA A;Residues: 1-3010 <KMT> A;Crose-references: UNIPROT:P26662; GB:D90208; NID:g221610; PIDN:BAA14233.1; PID:g22161 R;Kato, N.; Ohkoshi, S.; Shimotohno, K. Proc. Jpn. Acad. 65B, 219-223, 1989 A;Title: Japanese isolates of the non-A, non-B hepatitis viral genome show sequence var A;Reference number: PS0085

A; Accession: PS0086

Aprocession: 5207 - KRA2Aprocession: 5207 - KRA2Aprocession: 5207 - KRA2Aprocession: 5207 - KRA2Appearant of this polyprotein have not been determined.
C;Comment: The cleavage sites of this polyprotein
C;Comment: The cleavage sites of thi

F)1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F)1616-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F)2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F)2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F)196,209,234,250,305,325,417,423,430,448,532,556,576,623,645,1213,1255,2041,2077,2240,

Query Match Best Local Similarity 100. Matches 102; Conservative

2212 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVFSENKVVILDSFDPIRAVEDEREISVP 2271 1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 요 ઠે

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0; Gaps

0; Indels

2272 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 2313 61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102 g ò

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A; Accession: A38465
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N;Tanaka, T.; Kato, N.; Nakagawa, M.; Ootsuyama, Y.; Cho, M.J.; Nakazawa, T.; Hijikata, Viris Ree. 23, 39-53, 1992
A;Title: Molecular cloning of hepatitis C virus genome from a single Japanese carrier: B A;Reference number: A45573; MUID:92295714; PMID:1318627
A;Ross-references: UNIPROT:000269; GB:D11168; GB:D01171; NID:9221612; PIDN:BAA01943.1;
A;Ross-references: UNIPROT:000269; GB:D11168; GB:D01171; NID:9221612;
A;Ross-references: UNIPROT:000269; GB:D11168; GB:D01171; NID:9216120;
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: APP: Gylvoprotein; C#status predicted <NED>
F;20-115/Product: anoistructural protein NS1 #status predicted <NS2>
F;100-1615/Product: nonstructural protein NS4 #status predicted <NS3>
F;101-1307/Product: nonstructural protein NS4 #status predicted <NS3>
F;106-1307/Product: nonstructural protein NS4 #status predicted <NS3>
F;106-1301/Product: nonstructural protein NS5 #status predicted <NS3>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS3>
F;2014-3010/Product: 
                                                                                 polyprotein (clone 2206) - hepatitis C virus (isolate 22) (fragment)
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: PQ0250
C;Accession: PQ0250
B;Oshima, M.; Tsuchiya, M.; Yagasaki, M.; Orita, T.; Hasegawa, M.; Tomonoh, K.; Kojima, J. Gen. Virol. 72, 2805-2809, 1991
A;Title: cDNA clones of Japanese hepatitis C virus genomes derived from a single patient A;Reference number: PQ0245; MUID:92044457; PMID:1658209
A;Accession: PQ0250
A;Molecule type: genomic RNA
A;Accession: LONA coSH-
A;Coss-references: UNIPROT:Q9DTB3
C;Superfamily: hepatitis C virus genome polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome polyprotein - hepatitis C virus (strain JT)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
D;Contains: nonstructural protein NS49; nonstructural protein NS5
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
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90.2%; Pred. No. 7.7e-46;
______amarches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEILRRTRRFPPAIPVWARPDYNPPLIESWKDPDYVPPVVHG 194
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tes 94; Conservative
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Best Local Similarity 90.2
Matches 92; Conservative
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genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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A, Residues: 1-3010 <TAK>
A, Cross-references: UNIPROT: p26663; EMBL: MS8335; NID: g329770; PIDN: AAA72945.1; PID: g329.
C, Superfamily: hepatitis C virus genome polyprotein; glycoprotein; hydrolase; nonstructur: C, Keywords: ATP; capsid protein; envelope protein; glycoprotein; hydrolase; nonstructur: F; 121-131/Product: envelope protein B #status predicted <MED>
F; 192-189/Product: major envelope protein B #status predicted <MS1>
F; 300-729/Product: nonstructural protein MS2 #status predicted <MS2>
F; 1007-1615/Product: nonstructural protein MS2 #status predicted <MS2>
F; 1007-1615/Product: nonstructural protein MS2 #status predicted <MS2>
F; 11310-1137/Region: mucleotide-binding motif A (P-loop)
F; 11310-11317/Region: pEXH motif
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,2077,22
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N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructur
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
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A;Variety: isolate JK1
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: S18030; S33570; Ā48332; S18029
R;Honda, M.; Kaneko, S.; Massahi, U.; Kobayashi, K.; Murakami, S.
Submitted to the EMBL Data Library, September 1991
A;Pescription: A whole genome of hepatitis C virus cDNA was isolated from a single patir
A;Reference number: S18030
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R.Honda, M.; Kaneko, S.; Unoura, M.; Kobayashi, K.; Murakami, S.
Arch. virol. 128, 162-169, 1993
A.fitle: Sequence analysis of putative structural regions of hepatitis C virus isolated
A.Reference number: A48332; MUID:93119270; PMID:8380322
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A;Residues: 1-1010 <HON>
A;Cross-references: UNIPROT:Q68949; EMBL:X61596; NID:g59478; PIDN:CAA43793.1; PID:g5947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Title: Structure and organization of the hepatitis C virus genome isolated from human A,Reference number: A38465, MUID:91140698, PMID:1847440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.; Murakami, S.; Fujita, J.; Onishi,
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                                                                                                                                                                                                                                                                                                                                                                                                                              C,Species: hepatitis C virus
C,Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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Pred. No. 5.6e-44;
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                                        2272 AEILRKSKKFPPALPIWARPDYNPPLLESWKSPDYVPFAVHG 2313
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61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG
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91.2%; Pred. No. 5...
5; Mismatches
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R;Takamizawa, A.; Mori, C.; Fuke, I.; Manabe,
J. Virol. 65, 1105-1113, 1991
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Richen, P.J.; Lin, M.H.; Tai, K.F.; Liu, P.C.; Lin, C.J.; Chen, D.S.
Virology 188, 102-113, 1992
A;Title: The Taiwanse hepatitis C virus genome: sequence determination and mapping the A;Reference number: A40244; MUID:92230206; PMID:1314449
A;Accession: A40244
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F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
F;2014-309,233,234,250,305,325,417,423,430,448,532,540,556,576,623,645,1213,1255,2041,20
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A,Residues: 1-3011 cGHO-
A,Residues: 1-3011 cGHO-
A,Crose-references: UNTRROT:P26664; GB:M62321; NID:G329873; PIDN:AAA45676.1; PID:G32987
R,Crose. S.W.; McCmish, F.; Holmes, E.C.; Dow, B.; Peutherer, J.F.; Follett, E.; Yap, P.
J. Gen. Virol. 73, 1131-1141, 1992
A,Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to
A;Reference number: PQ0393; MUID:92268871; PMID:1316939
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A; Residues: 1577-1633 <CH2>
A; Experimental source: isolates B-b17
C; Superfamily: hepatitis C virus genome polyprotein
C; Keywords: ATP; capatid protein; envelope protein; glycoprotein; hydrolase; nonstructur
P;1-115/Product: capsid protein C #status predicted <CPC>
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N;Concains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (non protein NS4a; nonstructural protein NS4b; nonstructural protein NS5b; nonstructural protein NS4b; nonstructural protein NS5C; process: hepatitis C virus
C; paces: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C; Accession: A39166; PQ0403; PQ0404
R; Choo, Qi., Rchoman, K.H.; Han, J.H.; Berger, K.; Lee, C.; Dong, C.; Gallegos, Proc. Natl. Acad. Sci. U.S.A. 88, 2451-2455, 1991
A; Title: Genetic organization and diversity of the hepatitis C virus.
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                           Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
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Pred. No. 3.7e-43;
3; Mismatches 7; Indels
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1 Similarity 90.2%;
92; Conservative
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A, Residues: 1577-1633 <CHA>
A, Cross-references: DDBJ:D10128
host Homo sapiens (man)
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Best Local Similarity
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                                                                                 Accession: A40244
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Cispecies: hepatitis C virus
Cispecies: 11-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
Cispecies: Town P00248; P00249
Cispecies: Town P00248; P00249; P00249
Cispecies: Town P00248; P00249; P00249; P00249; P00249; P00249; P00249; P00248
A;Ritle: CDNA clones of Japanese hepatitis C virus genomes derived from a single patient A;Reference number: P00249; MUID:92044457; PMID:1658209
A;Accession: P00248
A;Molecule type: genomic RNA
A;Accession: P00248
A;Molecule type: genomic RNA
A;Cossion: P00248
C;Superfamily: hepatitis C virus genome Polyprotein
C;Superfamily: hepatitis C virus genome Polyprotein
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N;Contains: capaid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
                                                                                                                               A;Cross-references: EMEL:X61591
A;Note: this sequence is inconsistent with the nucleotide translation
A;Note: the authors translated the codon AGG for residue 43 as Pro, TGG for residue 320
as Trp, and TTC for residue 771 as Ser
A;Note: sequence extracted from NCBI backbone (NCBIN:121747, NCBIP:121748)
C;Superfamily: hepatitis C virus genome polyprotein
F;2-115/Product: capsid protein C #status predicted cDC>
F;116-191/Product: envelope protein E #status predicted cMES>
F;390-1006/Product: nonstructural protein NSI #status predicted cNS2>
F;1007-1615/Product: hepacivirin #status predicted cNS3>
F;1007-1615/Product: hepacivirin #status predicted cNS3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fil66-1862/Product: nonstructural protein NS4a #status predicted <N4A>
Fil63-2013/Product: nonstructural protein NS4b #status predicted <N4B>
Fil63-2014-3010/Product: nonstructural protein NS5 #status predicted <NS5>
Fil96,209,234,250,305,417,423,448,532,540,556,576,623,645/Binding site: carbohydrate (As
                  A;Accession: S33570
A;Molecule type: genomic RNA
A;Residues: 1-547,'T',549-621,'V',623-624,'S',626-652,'DL',655-761,'T',763-782 <HOW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2212 KATCTTRHDSPDADLIBANLLWRQEWGGNITRVESENKVVILDSFEPLRAEEDEREVSVA 2271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1230-1237/Region: nucleotide-binding motif A (P-loop)
1312-1317/Region: nucleotide-binding motif B
1316-1319/Region: DEXH motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 509; DB 2;
Pred. No. 6.4e-45;
6; Mismatches 4;
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tes 94; Conservative
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genome polyprotein - hepatitis C virus
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstruct)
protein NS4s; nonstructural protein NS4b; nonstructural protein NS5
(5,Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: $40770; PC1285
B;Okamoto, H.
submitted to the EMBL Data Library, March 1992
A;Reference number: $40770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:003463; EMBL:D10749; NID:9221586; PIDN:BAA01582.1; PID:92215
R;Okamoto, H.; Okada, S.; Sugiyama, Y.; Yotsumoto, S.; Tanaka, T.; Yoshizawa, H.; Tsuda, Dh. J. Exp. Med. 60, 167-177, 1990
A;Title: The S-terminal sequence of the hepatitis C virus genome.
A;Reference number: PC1284; MUID:91013116; PMID:2170712
A;Accession: PC1288
A;Accession: PC1288
A;Residues: 1-513 <OK2>
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A,Experimental source: isolate HC-J1
C,Superfamily: hepatitis C virus genome polyprotein
F;2-115/Product: capsid protein C #status predicted cCPC>
F;116-191/Product: major envelope protein E #status predicted cMES>
F;130-1006/Product: nonstructural protein NS1 #status predicted cNS1>
F;130-115/Product: nonstructural protein NS2 #status predicted cNS2>
F;1230-1237/Region: nucleotide-binding motif A (P-loop)
F;1317/Region: DEXH motif
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Species: negatitis C virus
C;Accession: P00252
R;Oshima, M.; Tsuchiya, M.; Vagasaki, M.; Orita, T.; Hasegawa, M.; Tomonoh, K.; Kojima, J. Gen. Virol. 72, 2805-2809, 1991
A;Title: cDNA clones of Japanese hepatitis C virus genomes derived from a single patient
A;Reference number: P00245; MUID:92044457; PMID:1658209
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C;Superfamily: hepatitis C virus genome polyprotein
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85.3%; Pred. No. 1.5e-39;
cive 7; Mismatches 8; Indels
                                                   2272 AEILRKSRRFADALPVWARPDYNPLLVETWKKDYEPPVVHG 2313
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A; Residues: 1-182 <OSH>
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A; Residues: 1-3011 < OKA>
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Best Local Similarity
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R;Inchauspe, G; Zebedee, S; Lee, D.H.; Sugitani, M; Nasoff, M.; Prince, A.M. submitted to GenBank, July 1992

A;Description: GenBank, July 1992

A;Description: Genemak, July 1992

A;Description: A5814

A;Reference number: A3814

A;Rocession: A38814

A;Ro
                                                                                                                                                                                                                                                                                                                                F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <N4B>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;205,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2077,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1616-1862/Product: nonstructural protein NS4a #status predicted <N4A>
F;1863-2013/Product: nonstructural protein NS4b #status predicted <NB>>
F;2014-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;204-3011/Product: nonstructural protein NS5 #status predicted <NS5>
F;196,209,234,305,325,417,423,430,448,476,532,540,556,576,623,645,1213,1255,2041,2240,23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome polyprotein - hepatitis C virus (strain H)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu
protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2212 KATCTANHDSPDAELIEANLLWRQEMGGNITRVESENKVVILDSFDPLVAEEDEREISVP 2271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP
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116-191/Product: envelope protein M #status predicted <EPM>192-389/Product: major envelope protein E #status predicted <MEE>1920-729/Product: nonstructural protein NS1 #status predicted <NS1>1930-1006/Product: nonstructural protein NS2 #status predicted <NS2>1930-1006/Product: nonstructural protein NS2 #status predicted <NS2>1930-1237/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
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84.3%; Pred. No. 1.2e-39;
iive 8; Mismatches 8;
                                                                                                                                                                                                                                                                                                      ,1316-1319/Region: DEXH motif
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Best Local Simil
Matches 87; C
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genome polyprotein - hepatitis C virus (isolate EUH1480)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS43; nonstructural protein NS45; nonstructural protein NS5
                                                                                                                                                                                          Cyspecies hepatitis C virus
C;Species hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: JCS620
R;Chamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A;Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant A;Reference number: JCS620; MUID:9736593; PMID:9223423
A;Accession: JCS620.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Nocecule type: mRNA
A; Residues: 1-3014 < CHAA
A; Residues: 1-3014 < CHAA
A; Residues: 1-3014 < CHAA
A; Cross-references: UNIPROT:039228; GB:Y13184
A; Cross-references: UNIPROT:039228; GB:Y13184
A; Experimental source: genotype 5a, which predominates in South Africa
A; Note: the translation of the nucleotide sequence is not complete in this paper
C; Superfamily: hepatitis C virus genome polyprotein
F; 121-15/Product: capsid protein M #status predicted < CPC>
F; 116-191/Product: envelope protein B #status predicted < NED>
F; 1392-389/Product: major envelope protein B; #status predicted < NSD>
F; 1308-1616/Product: nonstructural protein NS2 #status predicted < NS2>
F; 1308-1616/Product: nonstructural protein NS2 #status predicted < NS2>
F; 1313-1318/Region: nucleotide-binding motif B
F; 1313-1318/Region: nucleotide-binding motif B
F; 1313-1318/Region: DEXT motif
F; 1313-1318/Region: DEXT motif
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NyContains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstruct protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Accession: A40250; PQ0397; PQ0559
R;Okamoto, H.; Kurai, K.; Okada, S.I.; Yamamoto, K.; Lizuka, H.; Tanaka, T.; Fukuda, S Virology 188, 331-341, 1992
A;Title: Full-length sequence of a hepatitis C virus genome having poor homology to rep A;Reference number: A40250; MUID:92230232; PMID:1314459
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A,Residues: 1-3033 <OKA>
A,Residues: 1-3033 <OKA>
A,Residues: 1-3033 <OKA>
A,Residues: 1-3033 <OKA>
A,Cross-references: UNIPROT: P26661; GB: D10988; GB: D01221; NID: g221608; PIDN: BAA01761.1;
A,Cross-references: UNIPROT: P26661; GB: D10988; GB: D01221; NID: g221608; PIDN: BAA01761.1;
J. Gen. Virol. 73, 1131-1141, 1992
A,Title: Analysis of a new hepatitis C virus type and its phylogenetic relationship to A,Reference number: PQ0393; MUD: 92268871; PMID: 1316939
A,Accession: PQ0397
A,Accession: PQ0397
A,Residues: 2678-2754 <CHA>
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nes 70; Conserva
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Matches
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C;Species: hepatitis C virus
C;Species: J.Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Dete: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: PQ0253
S;Osbima, M.; Tsuchiya, M.; Yagasaki, M.; Orita, T.; Hasegawa, M.; Tomcnoh, K.; Kojima, J.; Can. Virol. 72, 2805-2809, 1991
A;Title: cDNA clones of Japanese hepatitis C virus genomes derived from a single patient A;Reference number: PQ0245; MUID:92044457; PMID:1658209
A;Accession: PQ0253
A;Molecule type: genomic RNA
A;Accession: L175 cOSH-
A;Residues: 1-175 cOSH-
A;Cross-references: UNIPROT:Q9DFE2; UNIPROT:Q9J3G2; UNIPROT:O89489; UNIPROT:Q68949; UNIPROT:C;Superfamily: hepatitis C virus genome Polyprotein
C;Keywords: polyprotein
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C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: PQ0251
R;Oshima, M.; Tsuchiya, M.; Yagasaki, M.; Orita, T.; Hasegawa, M.; Tomonoh, K.; Kojima, J. Gen. Virol. 72, 2805-2809, 1991
A;Title: cDNA clones of Japanese hepatitis C virus genomes derived from a single patient A;Reference number: PQ0245; MUID:92044457; PMID:1658209
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Pred. No. 3.5e-33;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 409; DB 2; Length 175;
Pred. No. 1e-34;
                                                             Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                          Indels
                                                         81.4%; Score 451; DB 2;
94.4%; Pred. No. 5.2e-39;
live 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Molecule type: genomic RNA
A,Residues: 1-173 <OSH>
A,Cross-references: UNIPROT:09QIY7; UNIPROT:09QIY2;
C,Superfamily: hepatitis C virus genome polyprotein
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                                                                                                                                                                                                                                                                                                                     61 AEILRKPRKFPPALPIWARPDYNPPLLESW 90
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153 AEILRRTRRFPPAIPVWARPD 173
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Best Local Similarity 88.9%;
Matches 72; Conservative 6
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94.0%;
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Best Local Similarity
                                                                                        Local Similarity
les 85; Conserv
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C;Keywords: polyprotein
C; Keywords: polyprotein
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                                                         Query Match
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A;Experimental source: isolate E-b12
R;Kato, N.; Ootsuyama, Y.; Ohkoshi, S.; Nakazawa, T.; Mori, S.; Hijikata, M.; Shimotohno Biochem Blophye. Res. Commun. 181, 279-285, 1991.
A;Title: Distribution of plural HCV types in Japan.
A;Reference number: PQ0554; MUID:92068204; PMID:1720309
A;Accession: PQ0559
A;Molecule type: mRNA
A;Residues: 2678-2729 KAT.
A;Cession: PQ0554; MUID:92068204; PMID:1720309
A;Accession: PQ0554; MUID:92068204; PMID:1720309
A;Accession: PQ0554; MUID:92068204; PMID:1720309
A;Residues: 2678-2729 KAT.
A;Cession: PRD:22000 FKD:2000 PKD:2000 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
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Search completed: August 12, 2005, 14:22:52 Job time : 22.2998 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KATCTTHHDSPDADLIEANL........NPPLLESWKDPDYVPPVVHG 102
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1612378 seqs, 512079187 residues
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Maximum Match 100%
Listing first 45 summaries
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Q6TZB5
Q6TZX2
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                           OM protein
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No.
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Q6tzh8 hepatitis c		Q6tziO hepatitis c							Q6tzj6 hepatítis c		Q6tzj8 hepatitis c	Q6tzk2 hepatitis c	Q6tzk3 hepatitis c
Детинв	Q6TZH9	267210	267212	O6TZI7	TZI8	Q6TZI9	TZJ3	TZJS	Qetzje	TZ37	OCTZJ8	Q6T2K2	26TZK3
_		_	Ī	_	2 06				2 06				2 06
254	254	254	254	254	254	254	254	254	254	254	254	254	254
0.96	96.0	96.0	96.0	0.96	0.96	96.0	96.0	96.0	0.96	96.0	0.96	0.96	0.96
532	532	532	532	532	532	532	532	532	532	532	532	532	532

# ALIGNMENTS

Gaps

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2212 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 2271
                                                                                                                    1 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPIRAVEDEREISVP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SERAIN=MD12;
STRAIN=MD12;
Nagayama K., Kurosaki M., Enomoto N., Miyasaka Y., Marumo F., Sato C.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF207753; AAF65943.1; -.
PIR; A61196; A61196.
PIR; PQ0246; PQ0246.
PIR; PS0329; PS0329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heparitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RASSP, GOUSTOSI; ICWX.

GO; GO: 0015028; ICWX.

R GO; GO: 0015028; C: viral capsid; IEA.

R GO; GO: 0015028; C: viral capsid; IEA.

R GO; GO: 0015028; C: viral capsid; IEA.

GO; GO: 0005128; F: ATP binding; IEA.

R GO; GO: 0005128; F: RATP binding; IEA.

R GO; GO: 0005128; F: RATP dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent helicase activity; IEA.

R GO; GO: 0005128; F: RATP-dependent replication; IEA.

R GO; GO: 0019079; F: viral genome replication; IEA.

R InterPro; IPR001345; CytC heme BS.

R InterPro; IPR001345; HCV core.

R InterPro; IPR001349; HCV env.

R InterPro; IPR001349; HCV RARP.

R InterPro; IPR001349; HCV RARP.

R InterPro; IPR001346; HCV RARP.

R InterPro; IPR001346; RNA pol EST Cys.

R InterPro; IPR00134; RNA pol EST Cys.

R InterPro; IPR00134; RNA pol EST Cys.

R InterPro; IPR00134; RNA pol EST Cys.

R Pfam; PP01543; HCV core; 1.

R Pfam; PP01543; HCV core; 1.
                                        DB 1; Length 3010;
                                    Query Match
100.0%; Score 554; DB 1; Length 3:
Best Local Similarity 100.0%; Pred. No. 3e-45;
Matches 102; Conservative 0; Mismatches 0; Indels
3010 AA; 327017 MW; AA993794F46DB185 CRC64;
                                                                                                                                                                                                                          2272 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 2313
                                                                                                                                                                                                     61 AEILRKPRKFPPALPIWARPDYNPPLLESWKDPDYVPPVVHG 102
                                                                                                                                                                                                                                                                                                                                                                    09JJIO;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 PRT; 3010 AA
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepacivirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polyprotein.
  SEQUENCE
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Pfam;
Pfam;
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                                                  | REMBLE, 1920208; AMA14233.1; -...
| REMBLE, 1920208; AMA14233.1; -...
| REROPS; 229.001; -...
| REROPS; 239.001; -...
| REROPS; 239.001; -...
| REROPS; 1039.001; -...
| REROPS; 1039.001; -...
| REROPS; 1039.001; -...
| REROPS; 1039.001; -...
| REPROPS; 1039.001; -...
| RICEPPO: IPRO0140; HCV_Capsid.
| RICEPPO: IPRO01551; HCV_Capsid.
| RICEPPO: IPRO01551; HCV_NS4D.
| RICEPPO: IPRO0140; HCV_NS4D.
| RICEPPO: IPRO0140; HCV_NS4D.
| RICEPPO: IPRO01650; Hellcase C.
| RICEPPO: IPRO01650; HCV_NS4D.
| REAM; PPO1540; HCV_NS21; I.
| REAM; PPO1540; HCV_NS21; I.
| REAM; PPO1550; HCV_NS4D; I.
| REAM; PPO1550; HCV_NS4D; I.
| REAM; PPO1550; HCV_NS5D; I.
| REAM; PPO1550; HCV_NS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Removed from capsid protein C by the cellular aminopeptidase.
Caplular aminopeptidase.
Capsid protein C (Potential).
Matrix protein (Potential).
Major envelope protein E (Potential).
Nonstructural protein NS1 (Potential).
Protease/helicase NS3 (Potential).
Nonstructural protein NS4 (Potential).
Nonstructural protein NS48 (Potential).
Nonstructural protein NS48 (Potential).
RNA-directed RNA polymerase (Potential).
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Charge relay system (By similarity)
Charge relay system (By similarity)
Charge relay system (By similarity)
ATP (Potential)
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  or send an email to license@isb-sib.ch)
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                             EMBL; D90208; BAA14233.1; -.
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64 KATCTTHHDSPDADLIEANLLWRQEMGGNITRVESENKVVILDSFDPLRAEEDEREVSVP 123
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Hepacivirus.
NCBI_TaxID=11103;
                                              Hepatitis C virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepativirus.
NCBI_TaxID=11103;
                                                                                                                                                                                                                                                                              96.8%; Score 536; DB 2; Length 254; 95.1%; Pred. No. 1.1e-44; ive 3; Mismatches 2; Indels
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Pred. No. 1.1e-44;
2; Mismatches 2; Indels
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; A7381681; AAQ86271.1; -.
InterPro; IRR02868; HCV NS5a.
                                                                                                                                             Puig-Basagoiti F., Saiz J.C., Forns X.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX381888; AAQ86478.1; -.
InterPro; IPR002668; HCV NS5a.
Pfam; Pf01506; HCV NS5a, 1.
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27148 MW; 6D26E3F416CA8189 CRC64;
                                                                                                                                                                                                                                                     254 AA; 27242 MW; 2B2F15FE832154ED CRC64;
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                       05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Created)
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1 Similarity 96.1%;
98; Conservative
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Name=NS5A;
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Matches 98
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ID Q6
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Hepacivirus.
NCBI_TaxID=11103;
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DOI=10.1128/JVI.76.21.11079-110990.2002;
DOI=in C., Herrmann B., Bruch K., Zeuzem S.;
"Hepatitis C. virus non-structural (NS)5A protein and interferon resistance: a new model for testing the reliability of mutational
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Last sequence update)
Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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98.0%; Pred. No. 1.8e-44;
Live 1; Mismatches 1;
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J. Virol. 76:11079-11090(2002).
EMBL: AJ507192; CAD45235.1; -.
InterPro; IPR002868; HCV NS5a.
Pfam; PF01506; HCV_NS5a; 1.
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01-MAR-2003 (TrEMBLrel. 23, Li
01-JUN-2003 (TrEMBLrel. 24, Li
Polyprotein (Fragment).
Hepatitis C virus.
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Length 254;

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Q6TZBS ID Q6 AC Q6 DT 05 DT 05

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Nagayama K., Kurosaki M., Bnomoto N., Miyasaka Y., Marumo F., Sato C.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF208024; AAF61205.1; -.

EMBL; AF208024; PIR; PQ0246.

PIR; PQ0246; PQ0246.

PIR; PS0329; PS0329.

HSSP; QBUYS1; ICWX.
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Pfam; PP01001; HCV N35a; 1.
Pfam; PP00701; Helicase C; 1.
Pfam; PP00798; Viral RdRP; 1.
SMART; SM00487; DEXDG; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Coat protein; Envelope protein; Glycoprotein; Nonstructural protein; Polyprotein; Transmembrane.
SEQUENCE 3008 AA; 326835 MW; 99AE09E14C3109F4 CRCf4.
                                                                                                                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
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GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019028; C:viral capsid; IEA.
GO; GO:0019024; F:ATP binding; IEA.
GO; GO:0008026; F:ATP binding; IEA.
GO; GO:0003723; F:RNA-dependent helicase activity; IEA.
GO; GO:0003926; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:000326; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:RNA-directed RNA polymerase activity; IEA.
GO; GO:0005198; F:Structural molecule activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
GO; GO:0006508; P:viral genome replication; IEA.
GO; GO:0019087; P:viral transformation; IEA.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                              PRT; 3008 AA
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InterPro; IPR004109; Peptidase S29.
InterPro; IPR004109; Peptidase S29.
InterPro; IPR002518; Pept Ser Cys.
InterPro; IPR007095; RNA pol DS PS.
InterPro; IPR007094; RNA pol DS PS.
InterPro; IPR007094; RNA pol DS PS.
Pfam; PF01549; HCV capsid; 1.
Pfam; PF01549; HCV core; 1.
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Interpro; IPR001410; DEAD.
Interpro; IPR001410; DEAD.
Interpro; IPR001522; HCV capsid.
Interpro; IPR002521; HCV capsid.
Interpro; IPR002521; HCV core.
Interpro; IPR002531; HCV core.
Interpro; IPR002531; HCV NS1.
Interpro; IPR001745; HCV NS4.
Interpro; IPR001496; HCV NS4D.
Interpro; IPR001496; HCV NS4D.
Interpro; IPR001496; HCV NS5A.
Interpro; IPR00166; HCV NSSA.
                                                                                                PRELIMINARY;
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fam; PF01006;
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MEDLINE-98295834; PubMed-9634077;
MEDLINE-98295834; PubMed-9634077;
MEDLINE-98295834; PubMed-9634077;
MEDLINE-98295834; PubMed-9634077;
ED F., Penin F., Wychowski C.;
Sequence analysis of the NS5A protein of European hepatitis C virus 1D isolates and relation to interferon sensitivity.";
Gen. Virol. 79:1373-1381(1998).
EMBL; AF033367; AAC41009-1; -..
FIR; PQ0252; PQ0252.
InterPro; IPR002868; HCV_NS5a.
Pfam; PP01506; HCV_NS5a.
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01-NOV-1998 (TrEMBLrel, 08, Last sequence update)
01-NOV-1998 (TrEMBLrel, 25, Last annotation update)
01-OCT-2003 (TrEMBLrel, 25, Last annotation update)
Polyprotein (Fragment)
Hepatitis C virus.
Niruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TAXID=11103;
                                                                 Viruses, ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus
NCBI_TaxID=11103;
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                                                                                                                                                      Puig-Basagoiti F., Saiz J.C., Forns X.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY301666; AAQ86256.1; -.
InterPro; IPR00268; HCV NSa.
PFam; PF01506; HCV_NSa:
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      sequence update)
annotation update)
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      05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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Matches 98; Conservative
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Matches 98; Conserval
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InterPro; IPR002868; HCV_NS5a.
Pfam; PF01506; HCV_NS5a; 1.
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NCBI_TaxID=11103;
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                                          Polyprotein.
NON TER
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SEQUENCE 44
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Hepatitis C virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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Hepacivirus.
NCBI_TaxID=11103;
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MEDLINE=22255437; PubMed=12368350;
DOI=10.1128/JVI.76.21.11079-11090.2002;
Sarrazin C., Herrmann E., Bruch K., Zeuzem S.;
"Hepatitis C virus non-structural (NS)5A protein and interferon resistance: a new model for testing the reliability of mutational
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                       Length 3008;
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                       Score 535; DB 2; Length 3C Pred. No. 2.2e-43; 3; Mismatches 2; Indels
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY381784; AAQ86374.1; -.
InterPro; IPR002868; HCV NSSa.
Pfam; PF01S06; HCV_NSSa; 1.
NON TER 254 254
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254 AA; 27064 MW; 1AB5FADB1EAF9CDD CRC64;
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Last sequence update)
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Last annotation update)
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EMBL; AJS07156; CAD45200.1; -.
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Best Local Similarity 95.19
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Matches 97; Conservative
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01-MAR-2003
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J. Virol. 76
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Hepacivirus.
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AA381869; AAQ86459-11;
InterPro; IRR02868; HCV NS5a.
Pfam; PF01506; HCV_NS5a; 1.
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                   non-structural protein 5A
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                                                           447 AA; 48586 MW; EE878DAEBEC97243 CRC64;
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Pred. No. 2.8e-44;
4; Mismatches 2;
                                                                                                  Score 533; DB 2;
Pred. No. 4.1e-44;
2; Mismatches 3;
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Name=NS5A
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Viruses; s8RNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
NCBI_TaxID=11103;
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96.0%; Score 532; DB 2; Length 254;
Best Local Similarity 94.1%; Pred. No. 2.8e-44;
Matches 96; Conservative 4; Mismatches 2; Indels
SEQUENCE FROM N.A.
Puig-Basagoiti F., Saiz J.C., Forns X.;
Puig-Basagoiti F., Saiz J.C., Forns X.;
Submitted (SEP-200, the EMBL/GenBank/DDBJ databases.
EMBL; AY381866; AAQ86456.1; -.
InterPro; IPR002868; HCV_NS5a.
Pfam; PF01506; HCV_NS5a; 1.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
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                                                                                                                                                                                            Length 254;
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94.1%; Pred. No. 2.8e-44;
iive 4; Mismatches 2; Indels
Puig-Basagoiti F., Saiz J.C., Forns X.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY381860; AAQ86450.1; -.
NON TER 11
NON TER 254 254
SEQUENCE 254 AA; 27252 MW; AEB6334960B77A9D CRC64;
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                                                                                                                                                                        Query Match
Best Local Similarity 94...
Best Local Similarity 94...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepacivirus.
NCBI_TaxID=11103;
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